

GenCore version 5.1.6  
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protein - protein search, using sw model

on: June 21, 2004, 17:21:47 ; Search time 22 Seconds  
(without alignments)  
950.387 Million cell updates/sec

File: US-09-095-478A-7  
Effect score: 405  
Sequence: 1 MSSPKVRKGTGRNDREEG.....DIMNIVTQMRKQRCGLQTX 405

oring table: OLIGO  
Gapop 60.0 , Gapext 60.0

arched: 389414 seqs, 51625971 residues

rd size : 0

tal number of hits satisfying chosen parameters: 389414

imum DB seq length: 0  
ximum DB seq length: 2000000000

st-processing: Listing first 100 summaries

atabase : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	15	3.7	272	US-08-446-345-34
2	15	3.7	1174	US-08-446-345-36
3	14	3.5	176	US-08-036-210-9
4	14	3.5	176	US-08-449-609-9
5	14	3.5	176	US-08-361-096A-9
6	14	3.5	245	US-08-685-992-26
7	14	3.5	245	US-09-144-925-26
8	14	3.5	289	US-09-361-096A-47
9	14	3.5	322	US-08-036-210-11
10	14	3.5	322	US-08-449-609-11
11	14	3.5	322	US-09-361-096A-11
12	14	3.5	401	US-09-361-096A-15
13	14	3.5	402	US-08-036-210-15
14	14	3.5	402	US-08-449-609-15
15	14	3.5	898	US-08-036-210-22
16	14	3.5	898	US-08-449-609-22
17	14	3.5	898	US-09-361-096A-22
18	14	3.5	1501	US-08-447-464-3
19	14	3.5	1501	US-08-716-679-3
20	14	3.5	1911	US-08-348-006B-5
21	14	3.5	1911	US-08-825A-5
22	14	3.5	1911	US-09-158-657-5
23	14	3.5	1911	PCT-US94-10566-5
24	12	3.0	245	US-08-015-985-8
25	12	3.0	245	US-09-280-597-8
26	12	3.0	257	US-08-685-992-18
27	12	3.0	257	US-09-144-925-18
28	12	3.0	263	US-08-685-992-5
29	12	3.0	263	US-09-144-925-5
30	12	3.0	1337	US-08-854-585-2
31	12	3.0	1337	US-09-447-533-2
32	12	3.0	1337	PCT-US95-05512-2
33	12	3.0	1442	US-08-015-986A-3
34	12	3.0	1442	US-08-446-363-3
35	12	3.0	1445	US-08-015-986A-2
36	12	3.0	1445	US-08-446-363-2
37	12	3.0	1711	US-08-342-930-2
38	11	2.7	11	US-08-342-930-4
39	11	2.7	235	US-08-015-985-5
40	11	2.7	235	US-09-280-597-5
41	11	2.7	236	US-08-015-985-6
42	11	2.7	242	US-09-280-597-6
43	11	2.7	242	US-08-015-985-7
44	11	2.7	242	US-09-280-597-7
45	11	2.7	248	US-08-015-985-9
46	11	2.7	248	US-09-848-294-10
47	11	2.7	248	US-09-280-597-9
48	11	2.7	250	US-08-685-992-7
49	11	2.7	250	US-08-685-992-24
50	11	2.7	250	US-09-144-925-7
51	11	2.7	250	US-09-144-925-24
52	11	2.7	253	US-08-685-992-10
53	11	2.7	253	US-08-685-992-11
54	11	2.7	253	US-09-144-925-10
55	11	2.7	253	US-09-144-925-11
56	11	2.7	254	US-08-685-992-9
57	11	2.7	254	US-08-685-992-14
58	11	2.7	254	US-08-685-992-23
59	11	2.7	254	US-09-144-925-9
60	11	2.7	254	US-09-144-925-14
61	11	2.7	254	US-09-144-925-23
62	11	2.7	255	US-08-685-992-16
63	11	2.7	255	US-09-144-925-16
64	11	2.7	257	US-08-685-992-6
65	11	2.7	257	US-09-144-925-6
66	11	2.7	260	US-08-685-992-4
67	11	2.7	260	US-08-685-992-25
68	11	2.7	260	US-09-144-925-4
69	11	2.7	260	US-09-144-925-25
70	11	2.7	261	US-08-685-992-3
71	11	2.7	261	US-09-144-925-3
72	11	2.7	277	US-08-685-992-22
73	11	2.7	277	US-09-144-925-22
74	11	2.7	278	US-08-201-697-16
75	11	2.7	289	US-08-036-210-13
76	11	2.7	289	US-08-449-609-13
77	11	2.7	289	US-09-361-096A-13
78	11	2.7	292	US-08-036-210-12
79	11	2.7	292	US-08-449-609-12
80	11	2.7	292	US-09-361-096A-12
81	11	2.7	699	US-08-348-006B-7
82	11	2.7	699	US-08-800-825A-7
83	11	2.7	699	US-09-158-657-7
84	11	2.7	793	US-08-015-985-3
85	11	2.7	793	US-09-280-597-3
86	11	2.7	802	US-08-015-985-1
87	11	2.7	802	US-09-280-597-1
88	11	2.7	1187	US-08-201-697-2
89	11	2.7	1188	US-08-201-697-4
90	11	2.7	1237	US-08-241-853-2
91	11	2.7	1237	US-08-850-917-2
92	11	2.7	2308	US-08-015-973-1
93	11	2.7	2308	US-08-448-164-1
94	11	2.7	2308	US-08-081-929-2
95	11	2.7	2314	US-09-816-703A-2
96	9	2.2	127	US-08-811-481-5
97	9	2.2	127	US-08-876-527-5
98	9	2.2	155	US-08-821-278A-17
99	9	2.2	231	US-08-446-345-37
100	9	2.2	242	US-08-685-992-21

## ALIGNMENTS

```

RESULT 1
US-08-446-345-34
Sequence 34, Application US/08446345
Patent No. 5831009
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683-054
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-446-345-34

Query Match 3.7%; Score 15; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 354 PLLVHCSAGVGRTGV 368
> 201 PLLVHCSAGVGRTGV 215
      |||||
      |||||

RESULT 2
US-08-446-345-36
Sequence 36, Application US/08446345
Patent No. 5831009
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683-054
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-446-345-36

Query Match 3.7%; Score 15; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 354 PLLVHCSAGVGRTGV 368
> 201 PLLVHCSAGVGRTGV 215
      |||||
      |||||

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; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,345
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,440
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 7683-054
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-446-345-36

Query Match 3.7%; Score 15; DB 2; Length 1174;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRTGV 368
DB 1103 PLLVHCSAGVGRTGV 1117
      |||||
      |||||

RESULT 3
US-08-036-210-9
; Sequence 9, Application US/08036210
; Patent No. 5385233
; GENERAL INFORMATION:
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,210
; FILING DATE: 23-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie

```

REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 176 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
I-08-036-210-9

Query Match 3.5%; Score 14; DB 1; Length 176;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGTGVFI 370  
79 VHCAGVGTGVFI 92

## RESULT 4

I-08-449-609-9  
Sequence 9, Application US/08449609  
Patent No. 5952212

## GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993

## ATTORNEY/AGENT INFORMATION:

NAME: Mistock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 176 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
I-08-449-609-9  
Query Match 3.5%; Score 14; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370  
Db 79 VHCAGVGTGVFI 92

## RESULT 5

US-09-361-096A-9  
Sequence 9, Application US/09361096A  
Patent No. 6492495

## GENERAL INFORMATION:

APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 176  
TYPE: PRT

## ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence  
OTHER INFORMATION: encoded by PCR fragment  
US-09-361-096A-9

Query Match 3.5%; Score 14; DB 4; Length 176;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370  
Db 79 VHCAGVGTGVFI 92

## RESULT 6

US-08-685-992-26  
Sequence 26, Application US/08685992  
Patent No. 5912138

## GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
S-08-685-992-26

Query Match 3.5%; Score 14; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 357 VHCSAGVGRGTGVFI 370  
Db 183 VHCSAGVGRGTGVFI 196

## RESULT 7

US-09-144-925-26  
Sequence 26, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
NUMBER OF INVENTIONS: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799

## COMPUTER READABLE FORM:

COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

## INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:  
LENGTH: 245 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
S-09-144-925-26

Query Match 3.5%; Score 14; DB 2; Length 245;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 357 VHCSAGVGRGTGVFI 370  
Db 183 VHCSAGVGRGTGVFI 196

## RESULT 8

US-09-361-096A-47  
Sequence 47, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:

APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 47  
LENGTH: 289  
TYPE: PRT

## ORGANISM: Artificial Sequence

## FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
US-09-361-096A-47

Query Match 3.5%; Score 14; DB 4; Length 289;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 357 VHCSAGVGRGTGVFI 370  
Db 221 VHCSAGVGRGTGVFI 234

## RESULT 9

US-08-036-210-11  
Sequence 11, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 322 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
IS-08-036-210-11

Query Match 3.5%; Score 14; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 357 VHCAGVGRGTGVPI 370  
|||  
b 221 VHCAGVGRGTGVPI 234  
|||

## RESULT 10

S-08-449-609-11  
Sequence 11, Application US/08449609  
Patent No. 5952212

## GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSES: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 322 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
IS-08-449-609-11

Query Match 3.5%; Score 14; DB 2; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
|||  
DB 221 VHCAGVGRGTGVPI 234  
|||

## RESULT 11

US-09-361-096A-11  
Sequence 11, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A

CURRENT FILING DATE: 1999-07-26  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 11  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

## OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D

US-09-361-096A-11

Query Match 3.5%; Score 14; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
|||  
DB 221 VHCAGVGRGTGVPI 234  
|||

## RESULT 12

US-09-361-096A-15  
Sequence 15, Application US/09361096A  
Patent No. 6492495  
GENERAL INFORMATION:

APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686

CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 15  
LENGTH: 401  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-361-096A-15

Query Match 3.5%; Score 14; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
|||  
DB 300 VHCAGVGRGTGVPI 313  
|||

```

RESULT 13
US-08-036-210-15
; Sequence 15, Application US/08036210
; Patent No. 5585233
; GENERAL INFORMATION:
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,210
; FILING DATE: 23-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-025
; TELEPHONE: 212-790-9090
; TELEFAX: 212-790-9090
; TELEX: 212-869-8864/9741
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-036-210-15

Query Match 3.5%; Score 14; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PY 357 VHCAGVGRGTGVFI 370
DB 301 VHCAGVGRGTGVFI 314

RESULT 14
US-08-449-609-15
; Sequence 15, Application US/08449609
; Patent No. 5952212
; GENERAL INFORMATION:
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,609
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/036,210
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-609-15

Query Match 3.5%; Score 14; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370
DB 301 VHCAGVGRGTGVFI 314

RESULT 15
US-08-036-210-22
; Sequence 22, Application US/08036210
; Patent No. 5585233
; GENERAL INFORMATION:
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,210
; FILING DATE: 23-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid

```

STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-22

Query Match 3.5%; Score 14; DB 1; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGTGVFI 370  
797 VHCAGVGTGVFI 810

## RESULT 16

US-08-449-609-22  
Sequence 22, Application US/08449609  
Patent No. 5952212

## GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel

TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995

## CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/036,210

## FILING DATE: 23-MAR-1993

## ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7683-025

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741

TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 22:

## SEQUENCE CHARACTERISTICS:

LENGTH: 898 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-449-609-22

Query Match 3.5%; Score 14; DB 2; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGTGVFI 370  
797 VHCAGVGTGVFI 810

## SULT 17

-09-361-096A-22  
Sequence 22, Application US/09361096A

Patent No. 6492495  
GENERAL INFORMATION:  
APPLICANT: MOLLER, NIELS P.H.  
APPLICANT: MOLLER, KARIN B.  
APPLICANT: ULLRICH, AXEL  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
FILE REFERENCE: 038602/0686  
CURRENT APPLICATION NUMBER: US/09/361,096A  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 08/449,609  
PRIOR FILING DATE: 1995-05-24  
PRIOR APPLICATION NUMBER: 08/036,210  
PRIOR FILING DATE: 1995-03-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 898  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTPS31-RD#2  
US-09-361-096A-22

Query Match 3.5%; Score 14; DB 4; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCAGVGTGVFI 370  
797 VHCAGVGTGVFI 810

## RESULT 18

US-08-447-464-3

Sequence 3, Application US/08447464

Patent No. 5840842

## GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph

APPLICANT: Yal, Hai

TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,464

FILING DATE: 24-MAY-1995

CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/130,570

FILING DATE: 01-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7683-043

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1501 amino acids

TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-447-464-3

Query Match 3.5%; Score 14; DB 2; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
Db 1431 VHCAGVGRGTGVFI 1444

RESULT 19  
US-08-716-679-3  
Sequence 3, Application US/08716679  
Patent No. 5846800  
GENERAL INFORMATION:  
APPLICANT: Schluesinger, Joseph  
APPLICANT: Yan, Hai  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN  
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/716,679  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/130,570  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-043  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-863-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1501 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-08-716-679-3

Query Match 3.5%; Score 14; DB 2; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 357 VHCAGVGRGTGVFI 370  
b 1431 VHCAGVGRGTGVFI 1444

RESULT 20  
S-08-348-006B-5  
Sequence 5, Application US/08348006B  
Patent No. 5658756  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.

APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,006B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J., MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 189521A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-348-006B-5

Query Match 3.5%; Score 14; DB 1; Length 1911;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
Db 1841 VHCAGVGRGTGVFI 1854

RESULT 21  
US-08-800-825A-5  
Sequence 5, Application US/08800825A  
Patent No. 5866397  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,825A  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-825A-5

Query Match 3.5%; Score 14; DB 2; Length 1911;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGTGVFI 370  
DB 1841 VHCSAGVGTGVFI 1854

RESULT 22  
US-09-158-657-5  
Sequence 5, Application US/09158657  
Patent No. 6214564  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/158,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/800,825  
FILING DATE: 14-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-158-657-5

Query Match 3.5%; Score 14; DB 3; Length 1911;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGTGVFI 370  
DB 1841 VHCSAGVGTGVFI 1854

RESULT 23  
PCT-US94-10166-5  
Sequence 5, Application PC/TUS9410166  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHN W. WALLEN III  
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10166  
FILING DATE: 09-SEPT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WALLEN, JOHN W III  
REGISTRATION NUMBER: 35403  
REFERENCE/DOCKET NUMBER: 18992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-10166-5

Query Match 3.5%; Score 14; DB 5; Length 1911;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGTGVFI 370  
DB 1841 VHCSAGVGTGVFI 1854

RESULT 24  
US-08-015-985-8  
Sequence 8, Application US/08015985  
Patent No. 553886  
GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
APPLICANT: Sap, Jan M.  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE

1 TITLE OF INVENTION: PHOSPHATASE-ALPHA  
2 NUMBER OF SEQUENCES: 14  
3 CORRESPONDENCE ADDRESS:  
4 ADDRESSEE: PENNIE & EDMONDS  
5 STREET: 1155 AVENUE OF THE AMERICAS  
6 CITY: NEW YORK  
7 STATE: NEW YORK  
8 COUNTRY: U.S.A.  
9 ZIP: 10036  
10 COMPUTER READABLE FORM:  
11 MEDIUM TYPE: Floppy disk  
12 COMPUTER: IBM PC compatible  
13 OPERATING SYSTEM: PC-DOS/MS-DOS  
14 SOFTWARE: Patent in Release #1.0, Version #1.25  
15 CURRENT APPLICATION DATA:  
16 APPLICATION NUMBER: US/08/015,985  
17 FILING DATE: 10-FEB-1993  
18 CLASSIFICATION: 435  
19 ATTORNEY/AGENT INFORMATION:  
20 NAME: Coruzzi, Laura A.  
21 REGISTRATION NUMBER: 30,742  
22 REFERENCE/DOCKET NUMBER: 7683-020  
23 TELEPHONE: (212) 790-9090  
24 TELEFAX: (212) 869-9741/8864  
25 TELEX: 66141 PENNIE  
26 INFORMATION FOR SEQ ID NO: 8:  
27 SEQUENCE CHARACTERISTICS:  
28 LENGTH: 245 amino acids  
29 TYPE: amino acid  
30 STRANDEDNESS: single  
31 TOPOLOGY: unknown  
32 MOLECULE TYPE: protein  
33 US-08-015-985-8  
34  
35 Query Match 3.0%; Score 12; DB 1; Length 245;  
36 Best Local Similarity 100.0%; Pred. No. 0.00087;  
37 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
38  
39 QY 356 LVHCSAGVGRGTG 367  
40 |||||  
41 Db 184 LVHCSAGVGRGTG 195  
42  
43 RESULT 25  
44 US-09-280-597-8  
45 Sequence 8, Application US/09280597  
46 Patent No. 6682905  
47 GENERAL INFORMATION:  
48 APPLICANT: Schlusser, Joseph  
49 APPLICANT: Sap, Jan M.  
50 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
51 TITLE OF INVENTION: PHOSPHATASE-ALPHA  
52 NUMBER OF SEQUENCES: 14  
53 CORRESPONDENCE ADDRESS:  
54 ADDRESSEE: PENNIE & EDMONDS  
55 STREET: 1155 AVENUE OF THE AMERICAS  
56 CITY: NEW YORK  
57 STATE: NEW YORK  
58 COUNTRY: U.S.A.  
59 ZIP: 10036  
60 COMPUTER READABLE FORM:  
61 MEDIUM TYPE: Floppy disk  
62 COMPUTER: IBM PC compatible  
63 OPERATING SYSTEM: PC-DOS/MS-DOS  
64 SOFTWARE: Patent in Release #1.0, Version #1.25  
65 CURRENT APPLICATION DATA:  
66 APPLICATION NUMBER: US/09/280,597  
67 FILING DATE:  
68 CLASSIFICATION:  
69 PRIOR APPLICATION DATA:  
70 APPLICATION NUMBER: US 08/015,985  
71 FILING DATE: 10-FEB-1993

1 ATTORNEY/AGENT INFORMATION:  
2 NAME: Coruzzi, Laura A.  
3 REGISTRATION NUMBER: 30,742  
4 REFERENCE/DOCKET NUMBER: 7683-020  
5 TELECOMMUNICATION INFORMATION:  
6 TELEPHONE: (212) 790-9090  
7 TELEFAX: (212) 869-9741/8864  
8 TELEX: 66141 PENNIE  
9 INFORMATION FOR SEQ ID NO: 8:  
10 SEQUENCE CHARACTERISTICS:  
11 LENGTH: 245 amino acids  
12 TYPE: amino acid  
13 STRANDEDNESS: single  
14 TOPOLOGY: unknown  
15 MOLECULE TYPE: protein  
16 US-09-280-597-8  
17  
18 Query Match 3.0%; Score 12; DB 4; Length 245;  
19 Best Local Similarity 100.0%; Pred. No. 0.00087;  
20 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
21  
22 QY 356 LVHCSAGVGRGTG 367  
23 |||||  
24 Db 184 LVHCSAGVGRGTG 195  
25  
26 RESULT 26  
27 US-08-685-992-18  
28 Sequence 18, Application US/08685992  
29 Patent No. 5912138  
30 GENERAL INFORMATION:  
31 APPLICANT: Tonke, Nicholas  
32 APPLICANT: Flint, Andrew J.  
33 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
34 TITLE OF INVENTION: TYROSINE PHOSPHATASES  
35 NUMBER OF SEQUENCES: 36  
36 CORRESPONDENCE ADDRESS:  
37 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
38 STREET: Two Militia Drive  
39 CITY: Lexington  
40 STATE: MA  
41 COUNTRY: USA  
42 ZIP: 02173  
43 COMPUTER READABLE FORM:  
44 MEDIUM TYPE: Diskette  
45 COMPUTER: IBM Compatible  
46 OPERATING SYSTEM: Windows 95  
47 SOFTWARE: FastSeq for Windows Version 2.0b  
48 CURRENT APPLICATION DATA:  
49 APPLICATION NUMBER: US/08/685,992  
50 FILING DATE: 25-JUL-1996  
51 CLASSIFICATION: 435  
52 PRIOR APPLICATION DATA:  
53 APPLICATION NUMBER:  
54 FILING DATE:  
55 ATTORNEY/AGENT INFORMATION:  
56 NAME: Granahan, Patricia  
57 REGISTRATION NUMBER: 32,227  
58 REFERENCE/DOCKET NUMBER: CSHL96-03  
59 TELECOMMUNICATION INFORMATION:  
60 TELEPHONE: 781-861-6240  
61 TELEFAX: 781-861-9540  
62 TELEX:  
63 INFORMATION FOR SEQ ID NO: 18:  
64 SEQUENCE CHARACTERISTICS:  
65 LENGTH: 257 amino acids  
66 TYPE: amino acid  
67 STRANDEDNESS: single  
68 TOPOLOGY: linear  
69 MOLECULE TYPE: peptide  
70 US-08-685-992-18  
71  
72 Query Match 3.0%; Score 12; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 0.00091;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
Db 187 LVHCSAGVGRGTG 198

## RESULT 27

US-09-144-925-18

Sequence 18, Application US/09144925

Patent No. 5951979

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02421-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,925

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,992

FILING DATE: July 25, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03Z

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

3-09-144-925-18

Query Match 3.0%; Score 12; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 0.00091;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
Db 187 LVHCSAGVGRGTG 198

## RESULT 28

-08-685-992-5

Sequence 5, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992

FILING DATE: 25-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-685-992-5

Query Match 3.0%; Score 12; DB 2; Length 263;

Best Local Similarity 100.0%; Pred. No. 0.00093;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
Db 193 LVHCSAGVGRGTG 204

## RESULT 29

US-09-144-925-5

Sequence 5, Application US/09144925

Patent No. 5951979

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02421-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,925

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,992

```

; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-144-925-5
Query Match 3.0%; Score 12; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367
Db 193 LVHCSAGVGRGTG 204

RESULT 30
US-08-854-585-2
; Sequence 2, Application US/08854585
; Patent No. 6114140
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K. and stman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,585
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27866/31954
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-854-585-2
Query Match 3.0%; Score 12; DB 3; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367

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Db 1236 LVHCSAGVGRGTG 1247

RESULT 31
US-09-447-533-2
; Sequence 2, Application US/09447533
; Patent No. 6552169
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
; PHOSPHATASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group PLLC
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 980104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/447,533
; FILING DATE: 23-NO. 6552169-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 200125.402C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-447-533-2
Query Match 3.0%; Score 12; DB 4; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367
Db 1236 LVHCSAGVGRGTG 1247

RESULT 32
PCT-US95-05512-2
; Sequence 2, Application PC/TUS9505512
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K. and stman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine
; PHOSPHATASE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 233 South Wacker Drive, Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05512  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27866/31954  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1337 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-05512-2

Query Match 3.0%; Score 12; DB 5; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
|||||

DB 1236 LVHCSAGVGRGTG 1247  
|||||

RESULT 33  
US-08-015-986A-3  
Sequence 3, Application US/08015986A  
Patent No. 5532123  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-GAMMA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/015,986A  
FILING DATE: 10-FEB-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7693-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1442 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-015-986A-3

Query Match 3.0%; Score 12; DB 1; Length 1442;

Best Local Similarity 100.0%; Pred. No. 0.0047;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 356 LVHCSAGVGRGTG 367  
|||||

DB 1054 LVHCSAGVGRGTG 1065  
|||||

RESULT 34  
US-08-446-363-3  
Sequence 3, Application US/08446363  
Patent No. 5891700  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-GAMMA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,363  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/015,986  
FILING DATE: 10-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7693-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1442 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-446-363-3

Query Match 3.0%; Score 12; DB 2; Length 1442;  
Best Local Similarity 100.0%; Pred. No. 0.0047;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
|||||

DB 1054 LVHCSAGVGRGTG 1065  
|||||

RESULT 35  
US-08-015-986A-2  
Sequence 2, Application US/08015986A  
Patent No. 5532123  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-GAMMA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/015,986A  
APPLICATION NUMBER: US/08/015,986A  
FILING DATE: 10-FEB-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-015-986A-2

Query Match 3.0%; Score 12; DB 1; Length 1445;  
Best Local Similarity 100.0%; Pred. No. 0.0047;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
DB 1057 LVHCSAGVGRGTG 1068

RESULT 36  
US-08-446-363-2  
Sequence 2, Application US/08446363  
Patent No. 5891700  
GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,363  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/015,986  
FILING DATE: 10-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-363-2

Query Match 3.0%; Score 12; DB 2; Length 1445;  
Best Local Similarity 100.0%; Pred. No. 0.0047;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
DB 1057 LVHCSAGVGRGTG 1068

RESULT 37  
US-08-342-930-2  
Sequence 2, Application US/08342930  
Patent No. 5821084  
GENERAL INFORMATION:  
APPLICANT: OLAMSTED, ELIZABETH A.  
APPLICANT: MAURO, LAURA J.  
APPLICANT: DAVIS, ALAN R.  
APPLICANT: DIXON, JACK E.  
TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/342,930  
FILING DATE: 21-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KONSKE, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20344-20975.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1711 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-342-930-2

Query Match 3.0%; Score 12; DB 2; Length 1711;  
Best Local Similarity 100.0%; Pred. No. 0.0055;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
DB 1347 LVHCSAGVGRGTG 1358

RESULT 38

US-08-342-930-4  
; Sequence 4, Application US/08342930  
; Patent No. 5821084  
; GENERAL INFORMATION:  
; APPLICANT: OLMSTED, ELIZABETH A.  
; APPLICANT: MAURO, LAURA J.  
; APPLICANT: DAVIS, ALAN R.  
; APPLICANT: DIXON, JACK E.  
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/342,930  
; FILING DATE: 21-NOV-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOSKI, ANTOINETTE F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 20344-20975.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; S-08-342-930-4

Query Match 2.7%; Score 11; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 357 VHCSAGVGRTG 367  
|||||  
b 1 VHCSAGVGRTG 11

RESULT 39  
S-08-015-985-5  
; Sequence 5, Application US/08015985  
; Patent No. 553886  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-ALPHA  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 AVENUE OF THE AMERICAS  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/280,597  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/015,985  
; FILING DATE: 10-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

US-08-015-985-5  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/015,985  
; FILING DATE: 10-FEB-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-015-985-5

Query Match 2.7%; Score 11; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRTG 367  
|||||  
DB 175 VHCSAGVGRTG 185

RESULT 40  
US-09-280-597-5  
; Sequence 5, Application US/09280597  
; Patent No. 6682905  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-ALPHA  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 AVENUE OF THE AMERICAS  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/280,597  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/015,985  
; FILING DATE: 10-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
IS-09-280-597-5

Query Match 2.7%; Score 11; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 357 VHCAGVGRGTG 367  
|||||  
b 175 VHCAGVGRGTG 185

## RESULT 41

IS-08-015-985-6  
Sequence 6, Application US/08015985  
Patent No. 5538886

GENERAL INFORMATION:  
APPLICANT: Schlensing, Joseph  
APPLICANT: Sap, Jan M.  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-ALPHA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10036

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/015,985  
FILING DATE: 10-FEB-1993  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-020  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO:

6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 236 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

IS-08-015-985-6

Query Match 2.7%; Score 11; DB 1; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 357 VHCAGVGRGTG 367  
|||||  
b 176 VHCAGVGRGTG 186

## RESULT 42

S-09-280-597-6

Sequence 6, Application US/09280597  
Patent No. 6682905

GENERAL INFORMATION:  
APPLICANT: Schlensing, Joseph  
APPLICANT: Sap, Jan M.  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE

TITLE OF INVENTION: PHOSPHATASE-ALPHA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/015,985  
FILING DATE: 10-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-020  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO:

6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 236 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-280-597-6

Query Match 2.7%; Score 11; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTG 367  
|||||  
Db 176 VHCAGVGRGTG 186

## RESULT 43

US-08-015-985-7

Sequence 7, Application US/08015985  
Patent No. 5538886

## GENERAL INFORMATION:

APPLICANT: Schlensing, Joseph  
APPLICANT: Sap, Jan M.

TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-ALPHA  
NUMBER OF SEQUENCES: 14

## CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10036

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/015,985  
FILING DATE: 10-FEB-1993  
CLASSIFICATION: 435



;; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
;; TITLE OF INVENTION: Adhesions and Uses Therefor  
;; FILE REFERENCE: CSHL90-04FZA  
;; CURRENT APPLICATION NUMBER: US/09/848,294  
;; PRIOR FILING DATE: 2001-05-03  
;; PRIOR APPLICATION NUMBER: 09/235,251  
;; PRIOR FILING DATE: 1999-01-22  
;; PRIOR APPLICATION NUMBER: 08/759,536  
;; PRIOR FILING DATE: 1996-12-04  
;; PRIOR APPLICATION NUMBER: 08/107,420  
;; PRIOR FILING DATE: 1993-08-16  
;; PRIOR APPLICATION NUMBER: 07/663,579  
;; PRIOR FILING DATE: 1991-03-01  
;; PRIOR APPLICATION NUMBER: 07/494,036  
;; PRIOR FILING DATE: 1990-03-14  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 10  
;; LENGTH: 248  
;; TYPE: PRT  
;; ORGANISM: Homosapiens  
US-09-848-294-10

Query Match 2.7%; Score 11; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.0087;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
|||  
DB 175 VHCAGVGRGTG 185

## RESULT 47

US-09-280-597-9  
; Sequence 9, Application US/09280597  
; Patent No. 6682905  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-ALPHA  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDWARDS  
; STREET: 1155 AVENUE OF THE AMERICAS  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/280,597  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/015,985  
; FILING DATE: 10-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7693-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid

;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; FEATURE:  
;; NAME/KEY: Modified-sites  
;; LOCATION: 1..248  
;; OTHER INFORMATION: /label=Xaa  
;; OTHER INFORMATION: /note="For the Consensus Sequence, Xaa = Lack of  
;; OTHER INFORMATION: Consensus"  
US-09-280-597-9

Query Match 2.7%; Score 11; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.0087;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
|||  
DB 188 VHCAGVGRGTG 198

## RESULT 48

US-08-685-992-7  
; Sequence 7, Application US/08685992  
; Patent No. 5912138  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,992  
; FILING DATE: 25-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 250 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-685-992-7

Query Match 2.7%; Score 11; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPPT 241  
|||  
DB 57 YIATQGLPPT 67

RESULT 49  
US-08-685-992-24  
Sequence 24, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-24  
Query Match 2.7%; Score 11; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
y 357 VHCAGVGRGTG 367  
b 180 VHCAGVGRGTG 190  
RESULT 50  
S-09-144-925-7  
Sequence 7, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA

ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-7  
Query Match 2.7%; Score 11; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 231 YIATQGLPET 241  
Db 57 YIATQGLPET 67  
RESULT 51  
US-09-144-925-24  
Sequence 24, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-24

Query Match 2.7%; Score 11; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
Db 180 VHCSAGVGRGTG 190

RESULT 52  
US-08-685-992-10  
Sequence 10, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-10

Query Match 2.7%; Score 11; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

357 VHCSAGVGRGTG 367  
|||||

Db 184 VHCSAGVGRGTG 194

RESULT 53  
US-08-685-992-11  
Sequence 11, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-11

Query Match 2.7%; Score 11; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
Db 184 VHCSAGVGRGTG 194

RESULT 54  
US-09-144-925-10  
Sequence 10, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA



357 VHCSAGVGR TG 367

Db 185 VHCSAGVGTG 195  
|||||

RESULT 57  
US-08-685-992-14

; Sequence 14, Application US/08685992  
; Patent No. 5912138  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,992  
; FILING DATE: 25-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-685-992-14

Query Match 2.7%; Score 11; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGTG 367  
Db 185 VHCSAGVGTG 195  
|||||

RESULT 58  
US-08-685-992-23

; Sequence 23, Application US/08685992  
; Patent No. 5912138  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington

QY 357 VHCSAGVGTG 367  
Db 185 VHCSAGVGTG 195  
|||||

RESULT 59  
US-09-144-925-9

; Sequence 9, Application US/09144925  
; Patent No. 5951979  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02421-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/144,925  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,992  
; FILING DATE: July 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227

; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,992  
; FILING DATE: 25-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-685-992-23

Query Match 2.7%; Score 11; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGTG 367  
Db 183 VHCSAGVGTG 193  
|||||

RESULT 59  
US-09-144-925-9

; Sequence 9, Application US/09144925  
; Patent No. 5951979  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02421-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/144,925  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,992  
; FILING DATE: July 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-9

Query Match 2.7%; Score 11; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
Db 185 VHCSAGVGRGTG 195

## RESULT 60

US-09-144-925-14  
Sequence 14; Application US/09144925  
Patent No. 5951979

GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-14

Query Match 2.7%; Score 11; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
Db 185 VHCSAGVGRGTG 195

## RESULT 61

US-09-144-925-23  
Sequence 23; Application US/09144925  
Patent No. 5951979

GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-23

Query Match 2.7%; Score 11; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
Db 183 VHCSAGVGRGTG 193

## RESULT 62

US-08-685-992-16  
Sequence 16; Application US/08685992  
Patent No. 5912138

GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive

Query Match 2.7%; Score 11; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-16

Query Match 2.7%; Score 11; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
DB 184 VHCSAGVGRGTG 194

RESULT 63  
US-09-144-925-16  
Sequence 16, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-16

Query Match 2.7%; Score 11; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
DB 184 VHCSAGVGRGTG 194

RESULT 64  
US-08-685-992-6  
Sequence 6, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-6

Query Match 2.7%; Score 11; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 357 VHCSAGVGRGTG 367  
|||||  
Db 188 VHCSAGVGRGTG 198

## RESULT 65

US-09-144-925-6  
; Sequence 6, Application US/09144925  
; Patent No. 591973  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02421-4799

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/144,925  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,992  
; FILING DATE: July 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; TELEX:

; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-144-925-6

Query Match 2.7%; Score 11; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 357 VHCSAGVGRGTG 367  
|||||  
b 188 VHCSAGVGRGTG 198

## RESULT 66

S-08-685-992-4  
; Sequence 4, Application US/08685992  
; Patent No. 5912138  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,992  
; FILING DATE: 25-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; TELEX:

; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 260 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-685-992-4

Query Match 2.7%; Score 11; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 357 VHCSAGVGRGTG 367  
|||||  
Db 191 VHCSAGVGRGTG 201

## RESULT 67

US-08-685-992-25  
; Sequence 25, Application US/08685992  
; Patent No. 5912138  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,992  
; FILING DATE: 25-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

APPLICANT: Tonks, Nicholas  
 APPLICANT: Flint, Andrew J.  
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
 TITLE OF INVENTION: TYROSINE PHOSPHATASES  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:

```

; ADDRESSES: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-992-3
;
; Query Match 2.7%; Score 11; DB 2; Length 261;
; Best Local Similarity 100.0%; Pred. No. 0.0091;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Y 357 VHCSAGVGRGTG 367
; | | | | |
; Db 192 VHCSAGVGRGTG 202
;
; RESULT 71
; US-09-144-925-3
; Sequence 3, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,992
; FILING DATE: July 25, 1996

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-144-925-3
;
; Query Match 2.7%; Score 11; DB 2; Length 261;
; Best Local Similarity 100.0%; Pred. No. 0.0091;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 357 VHCSAGVGRGTG 367
; | | | | |
; Db 192 VHCSAGVGRGTG 202
;
; RESULT 72
; US-08-685-992-22
; Sequence 22, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-992-22
;
; Query Match 2.7%; Score 11; DB 2; Length 277;

```





TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-036-210-13

Query Match 2.7%; Score 11; DB 1; Length 289;  
Best Local Similarity 100.0%; Pred.No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGPLEET 241  
Db 95 YIATQGPLEET 105

Search completed: June 21, 2004, 17:27:35  
Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 17:13:20 ; Search time 20 Seconds  
(without alignments)  
1947.878 Million cell updates/sec

Title: US-09-095-478a-7

Perfect score: 2133

Sequence: 1 MSSPRKVRGKTGRDNDREEG.....DIMNIVTQMKRQKCGMIQTK 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:.\*  
1: Pirl:.\*  
2: Pirl:.\*  
3: Pirl:.\*  
4: Pirl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	57.7	398	2 T08716	protein-tyrosine-p
2	603	28.3	2450	2 S71625	protein-tyrosine-p
3	597	28.0	2294	2 I67830	protein-tyrosine-p
4	597	28.0	2466	2 I67629	protein-tyrosine-p
5	589	27.6	2490	1 A54971	protein-tyrosine-p
6	477.5	22.4	1187	1 JC4155	protein-tyrosine-p
7	474	22.2	913	1 A41109	protein-tyrosine-p
8	456	21.4	1189	1 JC2366	protein-tyrosine-p
9	455	21.3	1337	1 I38670	protein-tyrosine-p
10	453	21.2	1997	1 S12050	protein-tyrosine-p
11	451	21.1	583	2 S17671	protein-tyrosine-p
12	450.5	21.1	1175	2 S51005	protein-tyrosine-p
13	449	21.1	1176	2 I58435	protein tyrosine p
14	448.5	21.0	2051	2 T30938	receptor tyrosine
15	446.5	20.9	926	1 A41105	protein-tyrosine-p
16	445	20.9	1174	2 I38140	protein-tyrosine-p
17	443	20.8	1238	2 S68700	HPTP beta-like tyr
18	442.5	20.7	387	1 A60345	protein-tyrosine-p
19	441.5	20.7	415	1 A33899	protein-tyrosine-p
20	441.5	20.7	1262	1 B48758	protein-tyrosine-p
21	441.5	20.7	1496	1 A48758	protein-tyrosine-p
22	440.5	20.7	1501	2 I58148	protein-tyrosine-p
23	440.5	20.7	1863	2 S46217	protein-tyrosine-p
24	440	20.6	1907	2 S50893	protein-tyrosine-p
25	439.5	20.6	1912	2 A56178	protein-tyrosine-p
26	439	20.6	1273	1 TDRILT	leukocyte common a
27	437.5	20.5	1118	1 A49724	protein-tyrosine-p
28	437	20.5	405	2 I49372	protein-tyrosine-p
29	437	20.5	597	2 B53978	protein-tyrosine-p

30 436 20.4 382 1 A38191 protein-tyrosine-p  
31 436 20.4 1188 1 A57064 protein-tyrosine-p  
32 436 20.4 1216 2 S60613 protein-tyrosine-p  
33 435 20.4 2314 1 A46151 protein-tyrosine-p  
34 434 20.3 363 1 S14294 protein-tyrosine-p  
35 434 20.3 1452 1 S17669 protein-tyrosine-p  
36 434 20.3 1457 1 A48066 hypotheical prote  
37 433.5 20.3 1156 2 T23308 protein-tyrosine-p  
38 433 20.3 694 2 A53978 protein-tyrosine-p  
39 432 20.3 405 2 S68250 protein-tyrosine-p  
40 432 20.3 1187 1 A53661 protein-tyrosine-p  
41 432 20.3 1291 1 A28334 protein-tyrosine-p  
42 432 20.3 1452 1 S17670 protein-tyrosine-p  
43 432 20.3 1459 2 I50212 protein-tyrosine-p  
44 430 20.2 1226 2 JC7503 protein-tyrosine-p  
45 427 20.0 1304 1 A46546 leukocyte common a

#### ALIGNMENTS

##### RESULT 1

T08716

protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999

C:Accession: T08716

R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: 216472

A:Accession: T08716

A:Molecule type: mRNA

A:Residues: 1-398 <ANS>

A:Cross-references: EMBL:AL050040

A:Experimental source: fetal kidney; clone DKFZp566K0524

C:Genetics:

A:Note: DKFZp566K0524.1

C:Superfamily: protein-tyrosine-phosphatase homology

P:161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 57.7%; Score 1231; DB 2; Length 398;

Best Local Similarity 64.9%; Pred. No. 3.4e-81;

Matches 238; Conservative 46; Mismatches 75; Indels 8; Gaps 2;

QY 40 PTKIFGKGNSENKPKSHLSFSDKYELVYPBLSDDTDVWDVSDSLRNWMS 99  
DB 18 PQAQVFENKVNSEKVKLSLRNFPHNDYEDVFESPSGSDPSMTARGPPFRDRWSSE 77  
QY 100 ETAGPSKTVSPVLSSGSRSLSKDTETSVSEKELTQAIQIRPLIENSARSAMRDLATLQK 159  
DB 78 EAAGPSQALSPLLS-----DTRKIVSEGLDQAIQIRPLIFNFHEQTAKDCKLLEE 130  
QY 160 K-BELDIIRFLELEQMTLPDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKNKYNAS 218  
DB 131 KTAAYDIQMFMALEKLNKLPGEVSGNQPSNRKNRYRDILPYDSTRVPLGSKDYNAS 190  
QY 219 YIRIVNHEEYFIATQGPETIEDFWQVNLNCNVIAMITREIECGVKKCVSWPIS 278  
DB 191 YIRIVNCGEEYFIATQGPLLSTIDDFWQVNLNNSNVIAMITREMEGGKIKYHWPI 250  
QY 279 LKPLETEHESVPLETFHTVQYTVRVFQIVKESGKSCQVHLQFTKPDHGTASADF 338  
DB 251 LKKPLELKHFRVFLNLYQILOYFIIRMFQVKESTGTSVSKQLQFTKPDHGTASADS 310  
QY 339 FIKTVRVKSHITGPLLHVCASGVTGTFICVDVVVFSALIKNYSPIIDNIVTQMKQR 398  
DB 311 FIKTVRVKSHITGPMVHCASGIGTGVFLCVDVVFCAIVKDCSFNIMDVAQMKRQR 370  
QY 399 CCMLOTK 405  
DB 371 SGMVQTK 377

## RESULT 2

S71625  
 A:Title: protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse  
 N:Alternate names: epidermal growth factor-binding protein; serine proteinase  
 C:Species: Mus musculus (house mouse)  
 C>Date: 27-Nov-1997 #sequence\_revision 12-Dec-1997 #text\_change 21-Jun-2002  
 C:Accession: S71625; S67987; I81209; I81209; S40290  
 R:Chida, D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T.  
 FEBS Lett. 358, 233-239, 1995  
 A:Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea  
 A:Reference number: S71625; MUID:95145716; PMID:7843407  
 A:Accession: S71625  
 A:Molecule type: mRNA  
 A:Residues: 1-2450 <CHI>  
 A:Cross-references: EMBL:D83966; NID:g1232103; PIDN:BAAL12158.1; PID:g1232104  
 A:Experimental source: strain DBA/2; cell line MEL 745A  
 R:Wolf, B.B.; Brown, M.D.  
 FEBS Lett. 376, 177-180, 1995  
 A:Title: Epidermal growth factor-binding protein activates soluble and receptor-bound si  
 A:Reference number: S67987; MUID:96105375; PMID:7498536  
 A:Accession: S67987  
 A:Molecule type: protein  
 A:Residues: 1098-1102 <WOL>  
 A:Experimental source: submaxillary glands  
 R:Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.  
 Science 268, 411-415, 1995  
 A:Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.  
 A:Reference number: I59595; MUID:95232528; PMID:7536343  
 A:Accession: I81210  
 A:Molecule type: mRNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1329-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>  
 A:Cross-references: GB:L34582; NID:g806297; PIDN:AA42056.1; PID:g806298  
 A:Accession: I81209  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1338-1354, 'K', 1356-1447, 'R', 1449-1454 <RE2>  
 A:Cross-references: GB:L34581; NID:g806295; PIDN:AA42055.1; PID:g806296  
 R:Hendrika, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 A:Reference number: S40280  
 A:Accession: S40290  
 A:Molecule type: mRNA  
 A:Residues: 2266-2372 <HEN>  
 A:Cross-references: EMBL:Z23059; NID:g438155; PIDN:CAA80594.1; PID:g438156  
 C:Genetics:  
 A:Gene: Ptpn13  
 A:Map position: 5  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros  
 F:566-860/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:1089-1165/Domain: GLGF domain homology <GLG1>  
 F:1361-1437/Domain: GLGF domain homology <GLG2>  
 F:1495-1574/Domain: GLGF domain homology <GLG3>  
 F:1769-1840/Domain: GLGF domain homology <GLG4>  
 F:1863-1937/Domain: GLGF domain homology <GLG5>  
 F:1863-1937/Domain: GLGF domain homology <GLG5>  
 F:2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:2374/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:2380/Binding site: substrate phosphate (Arg) #status predicted

Query Match 28.3%; Score 603; DB 2; Length 2450;  
 Best Local Similarity 31.6%; Pred. No. 8.7e-35;  
 Matches 157; Conservative 71; Mismatches 149; Indels 120; Gaps 13;

1 MSSP--KYRGKTGRDNDDEEGNSGLNLRSLPSSQKMTFTKPIFGNKNSENVRK---55

1952 ISAPRFTKANGLTSMK-----PSGQPALPKNSF--SKVNGGVHEAV 1992

56 -PSHLSPSKYEL-----VTFPELESSTDTVTVDVSDRSNRNWNM--97

1993 CPAGESSQMKESAGLTETKESNRDDDIYDDPOEAETVQSLDWDDEEAQNLLNQRHA 2052

QY 98 -----DSETAGPSKTVSPVLSGSSRLSK--- 120  
 Db 2053 TRACSPDLRTNGEAPEGDQYNGSPLEDPVPSVSSGEGKVDLASLTAASQBEKPIE 2112  
 QY 121 -----DTETS-----VSEKLTQLAQIRPLIFNSSARSAMRDCLNTLQ- 158  
 Db 2113 EDATGESRNSSTTETDGBDSSKDPPLTNEELALPVVVRVPSGKYTGQLQATIRTLQG 2172  
 QY 159 -----KKEELDIIRFLELEQMTLPDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKHK 212  
 Db 2173 LLDQIGPSKELNQLQELKPLDQCLI-----GQTKENRKNRYKNILPYDSTRVPLGDEG 2226  
 QY 213 DYINASYIRIVNHEEYFYIATQGLPETIEDFWOMLENNCNVIAMITRIEGVINYCY 272  
 Db 2227 GYNATFIRIPVGTQEFYIACQGLPTTVGDFWOMWQNSTVIAMMTQVEGEKIKCQ 2286  
 QY 273 SYWPISL-KEPLEFEPHPSVFLETFHTVQYFVTRVQIVKSGTSGSQCKVHLQFTKWPDHG 331  
 Db 2287 RWPSILGTTTMANERLALLRMQLKGFIVRMALEDIQTGEVRHSHLNFTAWPDHD 2346  
 QY 332 TPASAD---PFIKYRVYRKSHITGPLLHVSAGVGTGVFICVDVVPFSAIEKNYSFDIM 388  
 Db 2347 TFSQPDLLTPTSYMRHRRS---GPVITHCSAGIRSGTLICIDVVLGLISQDLFEDIS 2403  
 QY 389 NIVTQMRKQRCGMIOQTK 405  
 Db 2404 DLVRCWRLQRBHWQTE 2420  
 RESULT 3  
 I67630  
 A:Title: protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3  
 C:Species: Homo sapiens (man)  
 C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 30-Jun-2002  
 C:Accession: I67630  
 R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.  
 FEBS Lett. 337, 200-206, 1994  
 A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrai  
 A:Reference number: I53483; MUID:94116679; PMID:8287977  
 A:Accession: I67630  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2294 <RES>  
 A:Cross-references: GB:D21211; NID:g452193; PIDN:BA04752.1; PID:g452194  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;  
 C:Keywords: phosphoric monoester hydrolase  
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:1182-1258/Domain: GLGF domain homology <GLG2>  
 F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>  
 Query Match 28.0%; Score 597; DB 2; Length 2294;  
 Best Local Similarity 33.8%; Pred. No. 2.1e-34;  
 Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;  
 QY 6 KYRGKTGRDNDDEEGNSGLNLRSLP---SSSKMTFTKPIFGNKNSENVRKPSHLSF 62  
 Db 1898 KNGKLSERTEDTDCG-----SPLPEYFTETKNGCGEYCEKVKSESU----- 1944  
 QY 63 SKYELVPELESSTDTVTVDVSDRSLENNWNSMDSETAGPSKTVSPVLSGSSRLSKDT 122  
 Db 1945 -----IQKPEKKTDDDBITWG-NDELPFERTNEDSD-----KD- 1978  
 QY 123 ETSVSEKELTQLAQIRPLIFNSSARSAMRDCLNTLQ-----KKEELDIIRFLELEQ 175  
 Db 1979 HSFLTNDLAVLPVVKVLPSPGKYTGANLKSIVIRVLGLDQGIPSKELNQLQELKPDQC 2038  
 QY 176 TLPPDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQ 235  
 Db 2039 LI-----GQTKENRKNRYKNILPYDATRVPLGDEGYINASFKIPVSGKEFVLIACQ 2092  
 QY 236 GPLPETIEDFWOMLENNCNVIAMITRIEGVINYCYWPISL-KEPLEFEPHPSVFLET 294  
 Db 2093 GPLPTTVGDFWOMIWEQKSTVIAMMTQVEGEKIKCQRYWPNILGKTTWVSNRRLALVR 2152



```
QY 295 FHTQYFVTRVFOIVKMSKGSCQVKHLOFTKWDHGTTPASADFFIKYVYKSHLTGP 354
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2349 MOQLKGFVVRAMTLEIDITREVRHISHLFTANPDHPTQOPDLDLTFISYMHHRSGP 2408
QY 355 LLVHCSAGVGTGVPCVDVVFSAIEKNSFDIMNIVTQMKQKQCMQTK 405
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2409 IITHCSAGIGSGTLICIDVVLGLISQDLDFDISDLVRCMLQRHGVQTE 2459

RESULT 6
JC4155
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human
N/Alternate names: PEZ protein; protein-tyrosine-phosphatase/ezrin-like protein
C/Species: Homo sapiens (man)
C/Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
R/Accession: JC4155
R/Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.R.
Biochem. Biophys. Res. Commun. 209, 959-965, 1995
A/Title: PEZ: a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like dom
A/Reference number: JC4155; MUID:95251727; PMID:7733990
A/Molecule type: mRNA
A/Residues: 1-1187 <SM>
A/Cross-references: EMBL:X82676; NID:G929753; PIDN:CAAS7993.1; PID:9809029
A/Experimental source: breast
C/Genetics:
A/Gene: GDB:PTPN14
A/Cross-references: GDB:454485
A/Map position: lq32.2-lq32.2
C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F/23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
F/566-575/Region: proline-rich
F/709-716/Region: acidic
F/933-1169/Domain: protein-tyrosine-phosphatase homology <PTP>
F/1121/Active site: Cys (phosphocysteine intermediate) #status predicted
F/1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 22.4%; Score 477.5; DB 1; Length 1187;
Best Local Similarity 29.6%; Pred. No. 3.4e-26;
Matches 144; Conservative 67; Mismatches 152; Indels 123; Gaps 15;

QY 14 DNDDEEGNSGNLNLNSLPSSSQKMTPTKPIFGNKNSENKPKSHHSFSPKYLIVPEP 73
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
709 ESEEE-----ERAPESVQPIPMLEKREKMSYSAQQAALAIPIKRPPEYGP 755

QY 74 LESDTEVMDVSDRLNRKNSMDSETA-----GPSKTVS-----PVLSSGSS---R 117
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
756 RKS-----VSGALRQDQASLPAMARAVLRGPAKISMSTDPDPAVNGASLSPS 807

QY 118 LSKDRTTSVEK-----ELTQL-----AQIRPLIF 142
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
808 ISEPDLTSVKRVKPEPVSEMFLEDSIIIREMIRNLEKQKQVAGLEAKRPLML 867

QY 143 NS-----SARSAMDCNLTLOK-RELDIIRBFLBEOQLTPDDFNS 183
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
868 AALNGLSVARVSGREENRVDAFVMDERFRLKKLLEGWVFTEYEQIPKKANGIFST 927

QY 184 GNTLQNRDKRYRDILPYDSTRVPL-----GKNQYINASYIRIVNHESEYFIATQGLP 239
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
928 AALPENASRIRREVVPYENRVELLPTKENNTGTGINASHIKVYVVGGAEMHYIATQGLP 987

QY 240 ETIEDFWQVLENNKNCVIAITREICGVKICVSYWPISLKEPLEFHPSPVLETFHTQ 299
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
988 HTCHDFWQVWQGVNVIAVMTAEEGGRTKSHYWP-----KLGSKSSATYGVFKYTT 1042

QY 300 YFTVRVQIVKKS-----GKSCQVKGHLOFTKWDHGTTPASADFFIKY 344
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1043 KP--RTDSVCYATTGLKVHLLSQERTVHLOYTDWPHGCPEDVQGFSLYLBIOQVR 1100

QY 345 YVRKSHITG-----PLLVHCSAGVGTGVPCVDVVFSAIEKNSFDIMNIVTQMKQK 398
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1101 RHTNSMLEGTRKRRPPIVHCSAGVGTGVILSELMLICYLEHNEKEVPEVPMMLRLIREQR 1160
```

```
QY 399 CGMIQT 404
Db 1161 MFMIQT 1166
```

## RESULT 7

```
A41109
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - hum
N/Alternate names: PTPN3
C/Species: Homo sapiens (man)
C/Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002
R/Accession: A41109; I55698
R/Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A/Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with
A/Reference number: A41109; MUID:91296738; PMID:1648725
A/Accession: A41109
A/Molecule type: mRNA
A/Residues: 1-913 <YAN>
A/Cross-references: GB:M64572; NID:g179912; PIDN:AAA35647.1; PID:g179913
R/Ikuta, S.; Itoh, F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Imai, K.; Yachi, A.
J. Gastroenterol. 29, 727-732, 1994
A/Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPN1 mRNA
A/Reference number: I55698; MUID:95179278; PMID:7874267
A/Accession: I55698
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Cross-references: GB:I576309; NID:g913165; PIDN:AAB33583.1; PID:g913166
C/Genetics:
A/Gene: GDB:PTPN3
A/Cross-references: GDB:131386; OMIM:176877
A/Map position: 9q31-9q31
C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology,
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat
F/31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F/516-590/Domain: GLGF domain homology <GLG>
F/670-890/Domain: protein-tyrosine-phosphatase homology <PTP>
F/842/Active site: Cys (phosphocysteine intermediate) #status predicted
F/848/Binding site: substrate phosphate (Arg) #status predicted

Query Match 22.2%; Score 474; DB 1; Length 913;
Best Local Similarity 32.1%; Pred. No. 4.1e-26;
Matches 134; Conservative 60; Mismatches 156; Indels 68; Gaps 15;

QY 13 RNDDEEGNSGNLNLNSLPSSSQKMTPTKPIFGNKNSENKPKS--HHLSPSKYELVY 70
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
512 RITPDEDGKFG-FNLKGGV---DQKX---PLVWSRINPESPADTCIPKINEGDDQIVLIN 563

QY 71 FEPLESDTETVMDVSDRLNRKNSMDSETAGPSTVSPVLSSGSRSLSKDPTETSVSEKE 130
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
564 GRDISHTHDQV-----VMTIKASRSHSRELALVIRRAVRSFADFKSEDE 610

QY 131 LTQLAQIRPLIFNSSARSAMRDL--NTLQKKEBLDIREFLELRQM-----T 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
611 LNQL--FPEALFPMCPGEG--DTLEGSAQLKKGLESGTVLIQFQQLYRKPKGLAITFAK 666

QY 177 LPDDFNSGNTLQNRDKRYRDILPYDSTRVPLGKNKYINASYI-----RIVNHESEY 229
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
667 LP-----QMLDKNRFDVLPDPTTRVLVLOGEDYINASYVNMETPAANLVNK---- 713

QY 230 FYIATQGLPFIETIEDFWQVLENNKNCVIAITREICGVKICVSYWPISLKEPLEFPH-- 287
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
714 -YIATQGLPHTCAQSPQVQVMDQKLSLVMLATLTERTGRTKCHQYWP---DPPVMNHGG 769

QY 288 PSVLETFHTVQYFTVRVQIVKKSQCKVHLOFTKWDHGTTPASADFFIKYVYVR 347
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
770 FHTQCOSECDITAYVSRMLVNTVQTEGHTVTHLQYVAVPDHGLIPDDSSDFLEFNYVR 829

QY 348 KSHI--TGPLLVHCSAGVGTGVPCVDVVFSAIEKNSFDIMNIVTQMKQKQCMQTK 404
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
830 SLAVDSEPLVHCSAGIGTGVILVMTMETAMCLTERNLPIYPLDIVRKMGSDQAMMVQT 887
```

## RESULT 8

JC2366  
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse  
 N:Alternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phosphatase PTP36  
 C:Species: Mus musculus (house mouse)  
 C:Date: 24-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
 C:Accession: J02366  
 R:Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.  
 Biochem. Biophys. Res. Commun. 203, 479-484, 1994  
 A:Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskeletal protein-tyrosine-phosphatase  
 A:Reference number: JC2366; MUID:94354845; PMID:8074693  
 A:Accession: JC2366  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <SA>  
 A:Cross-references: GIB:D31842; MID:G507330; PIDN:BAA06628.1; PID:G507331  
 A:Experimental source: thymus  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-B  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:23-302/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:566-575/Region: proline-rich  
 F:712-718/Region: acidic  
 F:935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1123/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.4%; Score 456; DB 1; Length 1189;  
 Best Local Similarity 26.5%; Pred. No. 1.2e-24;  
 Matches 146; Conservative 73; Mismatches 149; Indels 182; Gaps 18;  
 Y 20 GNSGNLNR-----NSLPSSQKMT-----PTKPIPKNKNQENVK 55  
 b 636 GGGGVNKRHSLEVMNVMRGVNGEANTLKSINIPWARENTLREQPSSETGHEVHG--L 692  
 Y 56 PSHH--LSPSDYELVPEPELESDTDETVMDVSDR-----SLRNWNSM 97  
 b 693 POYHKHTFSDATMLHSS--ESSEBEETLBAAPQVPLREKVEYSNQLQALARPNP 750  
 Y 98 DSETAGPKTSPVLSGSRSLKSKOTE-----123  
 b 751 PPEYGPGRKSVS--NGALRQDQGTPLPAMARCRVLRHGFPSKALSVSRAQLAVNGASLG 807  
 Y 124 TGVSEKELTQL-----NSSARSARDCINTLQKKELDIIRFLEMTLPD-- 180  
 b 808 PSISEPDLTSYKRVKPEKVPKPERPVSFMSLEDSIIRRMNRLKQKWTGQQAQRPL 867  
 Y 141 IF-----NSSARSARDCINTLQKKELDIIRFLEMTLPD-- 180  
 b 868 MIAALNGLSVARVSGREDGRDTRVPIDERLRALKKLEDEM--FTEVEQ--IENKKA 923  
 Y 181 ----FNSGNTLQNRDKNRVRDILPYDSTRVPL-----GNKDYINASYIRIVNHEEYF 233  
 b 924 NGVFSTATLPENAESRIRFVVEENRVELIPTKENTGYINASHIKVVGSEWHYIA 983  
 Y 234 TQGPLPETIDFWQVLENNCNVNTAMTRETCEGVKCYSYNPISLKPLPEPHFSVLE 293  
 b 984 TQGPLPETIDFWQVLENNCNVNTAMTRETCEGVKCYSYNPISLKPLPEPHFSVLE 293  
 Y 294 TFWVTOYF-----TVRVFOIVKSKGSCVGHQFTKMPDHGTPASADPFIKY---- 342  
 b 1039 KFVYTKFTDUSGCVATGLKVKHLLSGQERTWHLQYTDWPHHGPEDEVQGLSVLEI 1098  
 Y 343 --VRVRSKSHITG-----PLLVHCSAGVGRGTGVCVDFVFAIKVYSFDMNITVQMKORCQGMIO 394  
 b 1099 QSVRHTNSVLEGRITRPHPIVHCSAGVGRGTGVCVDFVFAIKVYSFDMNITVQMKORCQGMIO 394  
 Y 395 RKQRCMIQT 404  
 b 1159 RQRMEMIQT 1168

## 35ULT 9

138670

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human  
 N:Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Mar-1996 #sequence\_revision 08-Mar-1996 #text\_change 22-Jun-1999  
 C:Accession: J38670; J52599  
 R:Postman, A.; Yang, Q.; Tonks, N.K.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994  
 A:Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced  
 A:Reference number: J38670; MUID:95024024; PMID:7937872  
 A:Accession: J38670  
 A:Molecule type: mRNA  
 A:Residues: 1-1337 <RES>  
 A:Cross-references: EMBL:U10886; MID:G558754; PID:G558755  
 A:Experimental source: HeLa cells  
 R:Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.  
 Blood 84, 4186-4194, 1994  
 A:Title: Molecular cloning, characterization, and chromosomal localization of a novel  
 A:Reference number: J52599; MUID:95086212; PMID:7994032  
 A:Accession: J52599  
 A:Status: preliminary; translated from GB/EXBL/DBBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-216; 'LFGVKAA', 225-260, 'G', 262-285, 'GTEGLDASNTERRA', 302, 'S', 304, 'TAPVH  
 A:Cross-references: GB:D37781; MID:G633072; PIDN:BAA07035.1; PID:G633073  
 C:Comment: Enhanced expression of this protein with increasing cell density suggests a  
 C:Genetics:  
 A:Gene: GDB:PTPRJ  
 A:Cross-references: GDB:385040; OMIM:600925  
 A:Map position: 19q33.4-19q33.4  
 C:Function:  
 A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III rep  
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tr  
 F:1-35/Domain: signal sequence #status predicted <SIG>  
 F:36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAJ  
 F:118-137/Domain: fibronectin type III repeat homology <3FNA>  
 F:206-283/Domain: fibronectin type III repeat homology <3FNB>  
 F:284-356/Domain: fibronectin type III repeat homology <3FND>  
 F:365-445/Domain: fibronectin type III repeat homology <3FNE>  
 F:453-530/Domain: fibronectin type III repeat homology <3FNF>  
 F:539-617/Domain: fibronectin type III repeat homology <3FNG>  
 F:720-804/Domain: fibronectin type III repeat homology <3FNG>  
 F:972-988/Domain: transmembrane #status predicted <TMN>  
 F:1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:122-82, 93, 104, 142, 172, 192, 231, 258, 278, 342, 353, 376, 391, 396, 413, 431, 501, 525, 536, 582, 603,  
 F:1239/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.3%; Score 455; DB 1; Length 1337;  
 Best Local Similarity 35.1%; Pred. No. 1.7e-24;  
 Matches 105; Conservative 56; Mismatches 110; Indels 28; Gaps 8;  
 Qy 119 SKDTETSVSEKELTQLAOTIRPLIFNSSARSARDCINTLQKKELD----IIRFLELEQ 174  
 Db 1003 AKNEVSFS-----QIKP-----KSKLIRVENFEAFKKQQAQSNCGFAEYEDLKL 1050  
 Qy 175 MTLDPDFNSGNTLQNRDKNRVRDILPYDSTRVPLG-----NKRDYINASYIRIVNHEEYF 230  
 Db 1051 VGISQPKYAAELAKNRKVRNNVLPYDISTRVPLSVQTHSTDDYINANVMPGYHKKD-- 1108  
 Qy 231 YIATQGLPETIDFWQVLENNCNVNTAMTRETCEGVKCYSYNPISLKPLPEPHPSV 290  
 Db 1109 FIATQGLPETIDFWQVLENNCNVNTAMTRETCEGVKCYSYNPISLKPLPEPHPSV 290  
 Qy 291 FLRTFHVTOYFTVRVFOIVKSKGSCVGHQFTKMPDHGTPASADPFIKY----VR-YV 346  
 Db 1167 AMTSEIVLPFWTIRDTFKVNIQTSESHPLRQPHFTSPWDHGVPTDILLINFRYLVRDY 1226  
 Qy 347 RKSHITGPIILVHCSAGVGRGTGVCVDFVFAIKVYSFDMNITVQMKORCQGMIO 405  
 Db 1227 KQSPSPILVHCSAGVGRGTGFIADIRLIYQIENENTVDVIGVIDURMRPLMVQTE 1285

## RESULT 10

S12050  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1993 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S12050; S15818; S15819  
R:Krueger, N.X.; Screuli, M.; Saito, H.  
EMBL J. 9, 3241-3252, 1990  
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases  
A:Reference number: S12049; MUID:9106019; PMID:2170109  
A:Accession: S12050  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1997 <KRU>  
A:CROSS-references: GB:X54131; NID:935787; PIDN:CAA38066.1; PID:935788  
FEBS Lett. 282, 285-288, 1991  
A:Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.  
A:Reference number: S15818; MUID:91243813; PMID:1645282  
A:Accession: S15818  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1872-1997 <VR2>  
C:Genetics:  
A:Gene: GDB:PTPRB; PTPB  
A:CROSS-references: GDB:127352; OMIM:176882  
A:Map position: 12q15.1-12q21  
A:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re  
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept  
F:1-22/Domain: signal sequence #status predicted <SI>  
F:23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <M  
F:1626-1642/Domain: transmembrane #status predicted <EXT>  
F:1643-1997/Domain: intracellular #status predicted <TM>  
F:1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:1904/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F:1910/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.24; Score 453; DB 1; Length 1997;  
Best Local Similarity 30.08; Pred. No. 4.2e-24;  
Matches 135; Conservative 62; Mismatches 161; Indels 92; Gaps 14;

QY 14 DNDEEGNGNMLRNLSLPSSQKMTPTKPIFGNKNSENVPKSHLSFSDKYL-- 69  
DB 1535 ENPNNSKSFNKLGAEMSLGKRPDQ-----QKCDGPKPHTAYRISIRATQLEDE 1590

QY 70 ----YPEPLESDTDTETVWDVSDRLNRNWSMDSETAGPSKTVSPVLSG----- 114  
DB 1591 DLKFTPLYSDTFSL-----PITSEPLFGAIEGVSGAGLFL 1629

QY 115 -----SSRLS--KDTETSYSEKELTOLAQIR---PLIFNSS 145  
DB 1630 IGLVAVVALLICQKVSHGRRPSPARLSIRDRPLSV-HLNLGQGNKRTSCPIKINQF 1688

QY 146 ARSARDCNLTLQKSELDIIRFLEQLQMTLPDPFNSGNTLQNRDKNRYRDIILPYDSTR 205  
DB 1689 BGHPMK-----LQADSNNLLSKEYEDLKDVGRSQSCDIALPENRGNKRYNNILPYDSTR 1743

QY 206 VPLGK-----NKQYINASYIRIVNHEEYFYIATQPLPETIEDFWQVLENNCNVIAMI 260  
DB 1744 VKLSNVDDPCSDYINASYIPGNFRRE--YIVTQGLPGTKDDFWKMWQNVHNVW 1801

QY 261 TRELECVIKYSWPLSLKEPLPEHPSVFLETHVQYFVTRVQIV-KKSTGKSCQCV 319  
DB 1802 TQCEKGRVKCDHWPAD-QDSLYYGLDILQMLSSVLPFWETIREFKICSEQDAHRLI 1860

QY 320 KHLQFTKWPDHGTSPASADFFIKYR-----YVRKSHITQPLLVHCSAGVGRGTGVFICVDVV 375  
DB 1861 RHPHYTVPDHPGVPETTSQSLIQFVRTVDRYINRSPGAGTVVHCSAGVGRGTGTFDALDRI 1920

## QY 376

376 PSALTEKNYSFDIMNIVTOMKORCGMIQTK 405  
DB 1921 LQQLDSKSDVDIYCAVHDLALHVRVHVQTE 1950

## RESULT 11

S17671  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Nov-1993 #sequence revision 15-Mar-1996 #text\_change 23-Jul-1999  
C:Accession: S17671; S40287  
R:Cebbink, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L  
FEBS Lett. 290, 123-130, 1991  
A:Title: Cloning, expression and chromosomal localization of a new putative receptor-1  
A:Reference number: S17669; MUID:92008644; PMID:1655529  
A:Accession: S17671  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-583 <GB>  
A:CROSS-references: EMBL:X58289  
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
submitted to the EMBL Data Library, June 1993  
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphat  
A:Reference number: S40280  
A:Accession: S40287  
A:Molecule type: mRNA  
A:Residues: 377-483, 'T' 485-486 <HEN>  
A:CROSS-references: EMBL:Z23056; NID:9438149; PIDN:CAA80591.1; PID:9438150  
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane pr  
F:11-536/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:488/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F:494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.18; Score 451; DB 2; Length 583;  
Best Local Similarity 29.58; Pred. No. 9.8e-25;  
Matches 131; Conservative 70; Mismatches 163; Indels 80; Gaps 14;

QY 14 DNDEEGNGNMLRNLSLPSSQKMTPTK-----PIFGNKNSENVPKSHLSFSDKYE 67  
DB 119 EPPSSSKSFNKLGAEMSLGKRPDQ-----PSPNPTT--ESEPLFGVIEGVSGAGLFLIGMLVA 178

QY 68 LVYPEPLESDTDTETVWDVSDRLNRNWSMDSETAGPSKTVSPVLSG----- 114  
DB 179 --FTKPLYSDT-----PSPNPTT--ESEPLFGVIEGVSGAGLFLIGMLVA 219

QY 115 -----SSRLS--KDTETSYSEKELTOLAQIR---PLIFNSSARSAMR 151  
DB 220 LVAFICQKASHRRPSPARLSIRDRPLSV-HLNLGQGNKRTSCPIKINOEGHPMK 278

QY 152 DCLNTLQKSELDIIRFLEQLQMTLPDPFNSGNTLQNRDKNRYRDIILPYDSTRVPLGK- 210  
DB 279 ----LQADSNNLLSKEYEDLKDVGRSQSCDIALPENRGNKRYNNILPYDASRVKLSNV 333

QY 211 ----NKQYINASYIRIVNHEEYFYIATQPLPETIEDFWQVLENNCNVIAMITREIEC 266  
DB 334 DDDPCSDYINASYIPGNFRRE--YIATQGLPGTKDDFWKMWQNVHNVWVQTCVEK 391

QY 267 GVTKYSWPLSLKEPLPEHPSVFLETHVQYFVTRVQIV-KKSTGKSCQCVKHLQFT 325  
DB 392 GRVKCDHWPAD-QDPLYTGDLILQMLSSVLPFWETIREFKICSEQDAHRLIRHFEYT 450

QY 326 KWPDHGTSPASADFFIKYR-----YVRKSHITQPLLVHCSAGVGRGTGVFICVDVPSALEK 381  
DB 451 WPDHPGVPETTSQSLIQFVRTVDRYINRSPGAGTVVHCSAGVGRGTGTFDALDRIILQQLDS 510

QY 382 NYSFDIMNIVTOMKORCGMIQTK 405  
DB 511 KDSVDIYGAVHDLALHVRVHVQTE 534

## RESULT 12

S51005  
 protein-tyrosine-phosphatase [EC 3.1.3.48] 2E - rat  
 C.Species: Rattus norvegicus (Norway rat)  
 C.Date: 10-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999  
 C.Accession: S51005; S51161  
 R.L.R. Abbe, D.; Banville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen, P.B.S. Lett. 356, 351-356, 1994  
 A.Title: Identification of a novel protein tyrosine phosphatase with sequence homology to PTP2B  
 A.Reference number: S51005; MUID:95104449; PMID:7805871  
 A.Accession: S51005  
 A.Molecule type: mRNA  
 A.Residues: 1-1175 <LAB>  
 A.Cross-references: EMBL:U17971; NID:96621113; PIDN:AAA62153.1; PID:9602255  
 A.Genetics: PTP2E  
 A.Accession: S51161  
 A.Molecule type: mRNA  
 A.Residues: 840-1175 <LAB>  
 A.Cross-references: EMBL:U18293; NID:9603228; PIDN:AAA62154.1; PID:9603229  
 A.Genetics: PTP2B1  
 A.Genetics: <PTP2E>  
 A.Note: clone PTP2E  
 A.Genetics: <PTP2B1>  
 A.Note: clone PTP2B1  
 C.Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-binding domain  
 C.Keywords: phosphoprotein, phosphoric monoester hydrolase, tyrosine-specific phosphatase  
 F:25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:922-1157/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1109/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.1%; Score 450.5; DB 2; Length 1175;  
 Best Local Similarity 28.2%; Pred. No. 2.9e-24;  
 Matches 141; Conservative 63; Mismatches 135; Indels 161; Gaps 17;  
 2Y 44 IFGNKMSNVKPK-----SHLSPDKYELVPELESDDTETVWVSDRLNRMNS 97  
 2b 677 VFSKVKQEGTEGGGSGYSHKSLSDATMLH-----SSDEE---DLEDDSSREHVA 729  
 2Y 98 DSEFAG-----PSKTVSPV-----LSGSSRLSKD-----TET 124  
 2b 730 PRLTAAPSQOQLNYPASVTPVTPGLHIFEPKSHVTFPEKRAKDIPVHLVMTHTOPRR 789  
 2Y 125 -----SVSEKLTQLAQIRPLIFNSSASAMRDCL-----NTIQ----- 158  
 2b 790 HGLTTPMSSESLLTTSGRV-----ARRDSLKKRPVSDLLSGKNTVEGLPLGG 839  
 2Y 159 -KKEELDIIR-----EFLEQWTLPPDFNSGNTL----- 187  
 2b 840 MKTRADAKKIGPLKLAALNGSLSLPLPDGKGVSTRAINDERCKVLEQRLQGTFT 899  
 2Y 188 -----QNRDKNRYRDLIPYDSTRVPLGKNKD-----YINASYIRI 222  
 2b 900 EYERILKRLVDGECSTARLPENAEARNRQDVLPPYDDARVELPTKENNTGYINASHIKV 959  
 2Y 223 VNHBEVEFYIATQGLPETIEQFMQWLENNCNVTAMITREICGVIKCYSYNPISLKEP 282  
 2b 960 SVSGIEWDYIATQGLPQNTQCDQFMQWVQGVALLIAMVTAEIEGREGKSPRYMP-----R 1014  
 2Y 283 LEPHFHVFLETHFTVYQYF-----TVRVFOIVKXSTKSCQVKHLQFTKWPDPHGTPAS 335  
 2b 1015 LGSRHNTVTVYGRFKITRTFRDTSGCCVATTGLKMKHLLTGQERTVWHLQYTDWPEHGCPED 1074  
 2Y 336 ADPFIKVRVYV-----RKSHITG-----PLLVHCSAGVGTGVFICVDVVFSALEKNYS 384  
 2b 1075 LKGFSLVLEIQSVRHTNSTSPSPNPLLVHCSAGVGTGVFVILSEIMVACLEHNEV 1134  
 2Y 385 FDIIMHVTQMRKQRCMIQT 404  
 2b 1135 LDIPRVLELLRQRMMLVQT 1154

RESULT 13  
 8345

protein tyrosine phosphatase - mouse  
 C.Species: Mus musculus (house mouse)  
 C.Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 22-Jun-1999  
 C.Accession: I58345  
 R.Higashitsuji, H.; Arai, S.; Furutani, M.; Inamura, M.; Kaneko, Y.; Takenawa, J.; Na Oncogene 10, 407-414, 1995  
 A.Title: Enhanced expression of multiple protein tyrosine phosphatases in the regenerating protein 4.1.  
 A.Reference number: I58345; MUID:95140431; PMID:7838537  
 A.Accession: I58345  
 A.Status: preliminary; translated from GB/EMBL/DDBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-1176 <RES>  
 A.Cross-references: GB:D37801; NID:9604885; PIDN:BA07053.1; PID:9604886  
 A.Genetics:  
 C.Gene: PTP-RL10  
 C.Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-binding domain  
 C.Keywords: phosphoprotein  
 F:25-304/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:923-1158/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1110/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1116/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.1%; Score 449; DB 2; Length 1176;  
 Best Local Similarity 28.5%; Pred. No. 3.8e-24;  
 Matches 138; Conservative 68; Mismatches 149; Indels 130; Gaps 16;  
 QY 44 IFGNKMSNVKPK-----SHLSPDKYELV-----YPELESDDT-DETVDVSDRLR 91  
 Db 677 VFSKVKQEGTEGGGSGYSHKSLSDATMLDSEEDDLEEDSSREQAISVSEPLT 736  
 QY 92 NRWN-----SMDSETAGP-----SKTVSPV-----LSGSSRLSKD--TET 124  
 Db 737 AAFQELNYPASATPTITGLHIFEPKSHVTFPEKRAKDIPVHLVMTHTPRDGLTTP 796  
 QY 125 SVSEKLTQLAQI-----RPLIFNSSASAMRDCLNTL--OKKEELDIIR----- 167  
 Db 797 SMSSEDLTTSGRVAREDSVKKAPVSDLLSGKKSAGEGLPLGGMKKTEADAKKIGPLK 856  
 QY 168 ---BFLSQWTLPPDFNSGNTL----- 187  
 Db 857 AALNGSLSLPLPDGKGVSTRAINDERCKVLEQRLQGTFTVYRILKRLVDGSCS 916  
 QY 188 -----QNRDKNRYRDLIPYDSTRVPLGKNKD-----YINASYIRI VNHBEVEFYIATQGLP 238  
 Db 917 TARLPENAEARNRQDVLPPYDDARVELPTKENNTGYINASHIKVSVSGIEWDYIATQGLP 976  
 QY 239 PETIEDFMQWLENNCNVTAMITREICGVIKCYSYNPISLKEPFEHPHVFLETHFTV 298  
 Db 977 QNTQCDQFMQWVQGVALLIAMVTAEIEGREGKSPRYMP-----RLGSRHNTVTVYGRFKIT 1031  
 QY 299 QYF-----TVRVFOIVKXSTKSCQVKHLQFTKWPDPHGTPASADPFIKVRVYV----- 347  
 Db 1032 TRFTDSCGYATTGLKMKHLLTGQERTVWHLQYTDWPEHGCPEDLKGFLSLEIQRV 1091  
 QY 348 -----KSHITG-----PLLVHCSAGVGTGVFICVDVVFSALEKNYSFIDIMHVTQMRKQRC 399  
 Db 1092 HTNSTSPKSH-NPPLLVHCSAGVGTGVFVILSEIMVACLEHNEVLDIPRVLDMLRQRM 1150  
 QY 400 GMIQT 404  
 Db 1151 MLVQT 1155

RESULT 14  
 T30938

receptor tyrosine phosphatase - medicinal leech  
 C.Species: Hirudo medicinalis (medicinal leech)  
 C.Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
 C.Accession: T30938  
 R.Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.  
 submitted to the EMBL Data Library, December 1997  
 A.Description: Two receptor tyrosine phosphatases of theLAR subfamily are expressed in



A:Reference number: Z20939

A:Accession: T30938

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2051 <GER>  
A:Cross-references: EMBL:AF017083; NID:g2695654; PID:g2695655; PIDN:AAB91460.1

C:Genetics:

A:Gene: LAR2

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

QGY

Query Match

Best local similarity 21.0%; Score 448.5; DB 2; Length 2051;

Matches 116; Conservative 69; Mismatches 129; Indels 65; Gaps 12;

37 KMTPTKIFGNKNSNVKPSHLSFSDKYLYWPELESDDTETVWDVSDRLNRWNS 96

1706 KHTGSVDIYGH-VTCLRAQRNVMVQTEDQYIFTHAILEAVTSGNT-EVPAENL----- 1757

97 MDSETAGPSTVSPVLSGSRSLSKDTSTVSEKLTQLAQIRPLFNSSARSAMDCLNT 156

1758 ----FAHQKLLLEP-LTITSQSGHSTTITGIEAEFKL-----SSGKTSL----- 1797

157 LQKKEELDIREFELEQWTLPPDFNSGNTLQNRDKNYRDILPYDSTRVPLG-----KN 211

1798 -----SSPASNLSCNKKQRLNVLVYETTRVCLQPIRGVDG 1835

212 KDYNASIVIRVNHSEYFVIATQGLPETIEDFQWVLENNCNVMIATREIBGVK 271

1836 SDYNASFD--GYRYRARIATQGLPETVEDFWALWESNCNIIIVMLTKLRGREN 1893

272 YSWPISLKEPLFEHESVF-LETFHTVQVFTVRVQIVKSKGSCQVKHLQFTKWDH 330

1894 HQWMP--SERSARVQYFVDPLEABYNPQVI-LREKAVTDARDQSRTRWQQLTDWPEQ 1950

331 GTPASADFFIKYRYVRKSH-----ITGLLVHCSAGVGRTPGVPCVDVVFSAIEKNYSF 386

1951 GVPSTGDFIDFIQTHKTKEQFQCEQPIAVHCSAGVGRTPGVITLSIVLERMFEGAYD 2010

387 IMNIVTQMRKQRCGMIOTK 405

2011 VFQTVNVLRTQPGNVQVTE 2029

RESULT 15

A41105 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human

N:Alternate names: Pirase MEG

C:Species: Homo sapiens (man)

C:Date: 20-Mar-1992 #sequence\_revision 02-May-1994 #text\_change 21-Jun-2002

C:Accession: A41105

R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.

Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991

A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty

A:Reference number: A41105; MUID:91288564; PMID:1648233

A:Accession: A41105

A:Molecule type: mRNA

A:Residues: 1-926 <GUA>

A:Cross-references: GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748

A:Experimental source: megakaryocytes, cell line MEG-10

C:Genetics:

A:Gene: GDB:PTPN4

A:Cross-references: GDB:131387; OMIM:176878

A:Map position: 9q31-9q31

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; F

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F:31-108/Domain: protein 4.1 membrane-binding domain homology <B41>

F:523-597/Domain: GLGF domain homology <GLG>

F:679-900/Domain: protein-tyrosine-phosphatase homology <FTP>

F:852/Active site: Cys (phosphocysteine intermediate) #status predicted

F:858/Binding site: substrate phosphate (Arg) #status predicted

Query Match

20.9%; Score 446.5; DB 1; Length 926;

Best Local Similarity 27.6%; Pred. No. 4e-24;  
Matches 121; Conservative 63; Mismatches 166; Indels 89; Gaps 9;

Qy 24 NLNRLNSLPSSSQKMTPTKPIFGNKNSENVPSPSHLSFSDKYLYWPELESDDTETVW 83

Db 490 HINETDIPSSPEKPTNGGIPHDNLVIRMKPDENGRFGFNKGYDQKMPVIVSRVA- 548

Qy 84 DVSDRSLRNRWNSMDSETAGPSKTSVPVLSGSRSLSKDTSTVSEKLTQLAQIRPLFN 143

Db 549 -----PQTPADLCVPLRNEGQVVLINGRDIAEHTHQVV---LPIK 587

Qy 144 SSARSAMRDCLNTLQKKEELDIIRPELE-----QMTLP 178

Db 588 ASCERESGELMLLVARNVAVDVVEKLENEPQFIPEKAPLDSVHQDDHSLSRESMIQLA 647

Qy 179 DDFNSGNTL-----QNRDKRYRDILPYDSTRVPLGKNQYINA 217

Db 648 EGIITGVLTQFDQLYRKPKGTMSCAKLPQNISKNRYHDISPYDATRVILKGNEDYINA 707

Qy 218 SYIR-----IVNHEEYFYIATQGLPETIEDFQWVLENNCNVMIATREIBGVK 270

Db 708 NYINMEIPSSIIHQ-----YIACQGLPHTCTDFWQMTWEGSSVMVMLTTQVERGRYK 762

Qy 271 CYSYWPISLKEPLFEHESVFLETFHTVQVFTVRVQ-----IVKSKGSCQVKHLQFTKW 327

Db 763 CHQYWP-----EPTGSSSYQCYQVTCHEEGNTAYIPKMTLFNQEKESRPLTQIQYIAW 818

Qy 328 PDHGTASADFFIKYRYVRKSHI--TGPLLHCSAGVGRTPGVPCVDVVFSAIEKNYSF 385

Db 819 PDHGVDPDSSDFLDFVCHVRNKEAGKEEPVWVHCSAGIGRTGVLITMETAMCLIECNQPV 878

Qy 386 DIMNIVTQMRKQRCGMIOQT 404

Db 879 YPLDIVRTMRDQRAMMIQT 897

Search completed: June 21, 2004, 17:18:57

Job time : 22 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 17:10:06 ; Search time 18 Seconds  
(without alignments)  
1171.578 Million cell updates/sec

Title: US-09-095-478a-7

Perfect score: 2133

Sequence: 1 MSSPRKVRGKTGRNDDEEG.....DIMNIVTQMKQRCGMQIQTK 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	28.0	2485	1 PTND_HUMAN	Q12923 homo sapien
2	477.5	22.4	1187	1 PTNE_HUMAN	Q15678 homo sapien
3	474	22.2	913	1 PTN3_HUMAN	P26045 homo sapien
4	456	21.4	1189	1 PTNE_MOUSE	Q62130 mus musculus
5	455	21.3	1337	1 PTPJ_HUMAN	Q12913 homo sapien
6	453	21.2	1997	1 PTPB_HUMAN	P23467 homo sapien
7	450.5	21.1	1175	1 PTNL_RAT	Q62728 rattus norv
8	449	21.1	1176	1 PTNL_MOUSE	Q62136 mus musculus
9	446.5	20.9	926	1 PTN4_HUMAN	P29074 homo sapien
10	445.5	20.9	1948	1 PTNS_HUMAN	Q13332 homo sapien
11	445	20.9	1174	1 PTNL_HUMAN	Q16825 homo sapien
12	443	20.8	1238	1 PTPJ_MOUSE	Q64455 mus musculus
13	442.5	20.7	1454	1 PTPF_MOUSE	Q99m80 mus musculus
14	442	20.7	1463	1 PTPF_HUMAN	Q14522 homo sapien
15	441.5	20.7	415	1 PTPD_HUMAN	P17706 homo sapien
16	439.5	20.6	1912	1 PTPD_MOUSE	P23468 homo sapien
17	439	20.6	1255	1 CD45_RAT	Q64157 rattus norv
18	438	20.5	2316	1 PTPZ_RAT	Q62656 rattus norv
19	436	20.4	382	1 PTPZ_MOUSE	Q06180 mus musculus
20	436	20.4	1216	1 PTPD_HUMAN	Q16827 homo sapien
21	435	20.4	1439	1 PTPK_HUMAN	Q15262 homo sapien
22	435	20.4	2314	1 PTP2_HUMAN	P23471 homo sapien
23	434	20.3	363	1 PTN2_RAT	P35233 rattus norv
24	434	20.3	1452	1 PTPK_HUMAN	P28827 homo sapien
25	434	20.3	1457	1 PTPK_MOUSE	P35822 mus musculus
26	432	20.3	1152	1 CD45_MOUSE	P05806 mus musculus
27	432	20.3	1452	1 PTPM_MOUSE	P28828 mus musculus
28	427	20.0	1304	1 CD45_HUMAN	P08575 homo sapien
29	426.5	19.9	434	1 PTN1_CHICK	Q13016 gallus gall
30	424.5	19.9	1026	1 PTP1_CAEEL	P28191 caenorhabdi
31	422	19.8	2200	1 LAR_CAEEL	Q9bm8 caenorhabdi
32	421.5	19.8	1897	1 PTPF_HUMAN	P10586 homo sapien
33	420	19.7	377	1 PTPF_DICTDI	P34138 dictyostell

#### ALIGNMENTS

##### RESULT 1

ID	PTND_HUMAN	STANDARD;	PRT; 2485 AA.
AC	Q12923; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q81WH7;		
AC	Q9NYN9;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)		
DE	(protein-tyrosine phosphatase 1E) (PTP-E1) (hPTPGL) (PTP-BAS)		
DE	(protein-tyrosine phosphatase PTP11) (Pas-associated protein-tyrosine phosphatase 1) (PAP-1)		
DE	phosphatase 1) (PAP-1)		
GN	PTPN13 OR PTP1E OR PTP11 OR PNP1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 4).		
RC	TISSUE=Breast carcinoma;		
RX	MEDLINE=94350988; PubMed=8071359;		
RA	Banville D., Ahmad S., Stocco R., Shen S.-H.;		
RT	"A novel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated		
RT	guanylate kinases.";		
RL	J. Biol. Chem. 269:22320-22327(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.		
RC	TISSUE=Leukemia;		
RX	MEDLINE=94116579; PubMed=8287977;		
RA	Maekawa K., Imagawa N., Nagamatsu M., Harada S.;		
RT	"Molecular cloning of a novel protein-tyrosine phosphatase containing		
RT	a membrane-binding domain and GLOF repeats.";		
RL	FEBS Lett. 337:200-206(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fibroblast;		
RX	MEDLINE=95014139; PubMed=7929060;		
RA	Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;		
RT	"Cloning and characterization of PTP11, a protein tyrosine phosphatase		
RT	with similarities to cytoskeletal-associated proteins.";		
RL	J. Biol. Chem. 269:24082-24089(1994).		
RN	[4]		
RP	SEQUENCE OF 1216-2490 FROM N.A.		
RC	TISSUE=Pancreas;		
RA	Wang H.Y.;		
RT	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.		
RL	[5]		
RP	SEQUENCE OF 1279-1893 FROM N.A. (ISOFORM 4).		
RC	TISSUE=Brain;		
RX	MEDLINE=95232528; PubMed=7536343;		
RA	Sato T., Irie S., Kitada S., Reed J.C.;		
RT	"PAP-1: a protein tyrosine phosphatase that associates with Pas.";		
RL	Science 268:411-415(1995).		
RN	[6]		
RP	SEQUENCE OF 1323-1821 FROM N.A.		

34	418	19.6	435	1	PTN1_HUMAN	P18031 homo sapien
35	418	19.6	780	1	PTNC_HUMAN	Q05209 homo sapien
36	416.5	19.5	360	1	PTN7_HUMAN	P35236 homo sapien
37	414	19.4	432	1	PTN1_RAT	P20417 rattus norv
38	413	19.4	1445	1	PTPG_HUMAN	P23470 homo sapien
39	412	19.3	432	1	PTN1_MOUSE	P35821 mus musculus
40	410	19.2	775	1	PTNC_MOUSE	P35831 mus musculus
41	409	19.2	1705	1	PTPV_MOUSE	P70289 mus musculus
42	406.5	19.1	359	1	PTN7_RAT	P49445 rattus norv
43	405	19.0	593	1	PTNB_CHICK	Q90687 gallus gall
44	405	19.0	1711	1	PTPV_RAT	Q64612 rattus norv
45	403.5	18.9	593	1	PTNB_RAT	P41499 rattus norv

RA Irie S., Hachiya T., Sato T.A.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RC TISSUE=Eye  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Matek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.Y., Skalek U., Smailus D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
 RN [8]  
 RP INTERACTION WITH TRIP6.  
 RX MEDLINE=99329089; PubMed=10400701;  
 RA Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;  
 RL "ZRP-1, a tyrosine-related protein, interacts with the second PDZ domain  
 of the cytosolic protein tyrosine phosphatase hPTP1B.";  
 RL J. Biol. Chem. 274:20679-20687(1999).  
 RN [9]  
 RP INTERACTION WITH NGFR.  
 RX MEDLINE=20012928; PubMed=10544233;  
 RA Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,  
 RA Reed J.C., Bradesen D.E., Sato T.A.;  
 RL "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with  
 p75(NTR) and their effect on NF-kappaB activation.";  
 RL FEBS Lett. 460:191-198(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE  
 C-TERMINUS OF TNFRSF6.  
 RX MEDLINE=20170882; PubMed=10704206;  
 RA Kozlov G., Gehring K., Ekiel I.;  
 RL "Solution structure of the PDZ2 domain from human phosphatase hPTP1B  
 and its interactions with C-terminal peptides from the Fas  
 receptor.";  
 RL Biochemistry 39:2572-2580(2000).  
 RN [11]  
 RP STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE  
 GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEP-2.  
 RX MEDLINE=22090786; PubMed=12095257;  
 RA Kozlov G., Banville D., Gehring K., Ekiel I.;  
 RL "Solution structure of the PDZ2 domain from cytosolic human  
 phosphatase hPTP1B complexed with a peptide reveals contribution of  
 the beta2-beta3 loop to PDZ domain-ligand interactions.";  
 RL J. Mol. Biol. 320:813-820(2002).  
 RN [12]  
 RP VARIANTS PRO-1419 AND MET-1522.  
 RX MEDLINE=22323362; PubMed=12436199;  
 RA Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Ekiel I.;  
 RL "Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)  
 and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and  
 seven polymorphisms of the FAP-1 gene.";  
 RL J. Hum. Genet. 41:614-619(2002).  
 RN [13]  
 RP FUNCTION: Regulates negatively Fas-induced apoptosis and NGFR-  
 mediated pro-apoptotic signaling.  
 RC CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 tyrosine + phosphate.  
 RC SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through  
 its second PDZ domain. Interacts with the C-terminal SVP motif of

NGFR through its third PDZ domain.  
 -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 -1- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=4;  
 Name=1;  
 IsoId=Q12923-1; Sequence=Displayed;  
 Name=2;  
 IsoId=Q12923-2; Sequence=VSP\_000496;  
 Name=3;  
 IsoId=Q12923-3; Sequence=VSP\_000497;  
 Name=4;  
 IsoId=Q12923-4; Sequence=VSP\_007921;  
 Note=May be due to a competing donor splice site;  
 TISSUE SPECIFICITY: Present in most tissues with the exception of  
 the liver and skeletal muscle. Most abundant in lung, kidney and  
 fetal brain.  
 -1- SIMILARITY: Contains 1 FERM domain.  
 -1- SIMILARITY: Contains 5 PDZ/DHR domains.  
 -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 Non-receptor class subfamily.  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 EMBL: U12128; AAB60339.1;  
 EMBL: D21209; BAA04750.1;  
 EMBL: D21210; BAA04751.1;  
 EMBL: D21211; BAA04752.1;  
 EMBL: X80289; CAA56563.1;  
 EMBL: X79676; CAA56124.1;  
 EMBL: L34583; AAC41755.1;  
 EMBL: AF23323; AAF63474.1;  
 EMBL: BC039610; AAH39610.1; ALT\_TERM.  
 PIR: A54971; A54971.  
 PIR: I67629; I67629.  
 PIR: I67630; I67630.  
 PDB: 1PDZ; 17-MAR-00.  
 PDB: 1DSG; 24-JUL-02.  
 Genes: HGNC:9646; PTFN13.  
 MIM: 600267;  
 GO: 0004725; P:protein tyrosine phosphatase activity; TAS.  
 GO: 0006470; P:protein amino acid dephosphorylation; TAS.  
 InterPro: IPR000299; Band\_4.1.  
 InterPro: IPR001478; PDZ.  
 InterPro: IPR000367; Tyr\_phosphatase.  
 InterPro: IPR000242; Tyr\_PP.  
 Pfam: PF00373; Band\_41; 1.  
 Pfam: PF00595; PDZ; 5.  
 Pfam: PF0102; Y\_phosphatase; 1.  
 PRINTS: PR00935; BAND41.  
 PRINTS: PR00700; PRTYPHPTASE.  
 SMART: SM00295; B41; 1.  
 SMART: SM00228; PDZ; 5.  
 SMART: SM00194; FPG1; 1.  
 PROSITE: PS00660; FERM\_1; FALSE\_NEG.  
 PROSITE: PS00661; FERM\_2; FALSE\_NEG.  
 PROSITE: PS00557; FERM\_3; 1.  
 PROSITE: PS0106; PDZ; 5.  
 PROSITE: PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
 PROSITE: PS00383; TYR\_PHOSPHATASE\_2; 1.  
 PROSITE: PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
 Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure;  
 Alternative splicing; Coiled coil; Polymorphism.  
 DOMAIN 56 59  
 DOMAIN 572 872  
 DOMAIN 2237 2485  
 DOMAIN 379 399  
 DOMAIN 469 504

DR	EXBL; X82676; CAA57993.1; -.
DR	PIR; JC4155; JC4155.
DR	HSP; P29350; IGNZ.
DR	Genew; HGNC:9647; PTPN14.
DR	MIM; 603155; -.
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR	InterPro; IPRO00299; Band 4.1.
DR	InterPro; IPRO00387; TYR_PSPHATASE.
DR	InterPro; IPRO00242; TYR_PP.
DR	Pfam; PF00373; Band 41; 1.
DR	Pfam; PF00102; Y_phosphatase; 1.
DR	PRINTS; PR00935; BAND41.
DR	PRINTS; PR00700; PTYPHPHTASE.
DR	SMART; SM00295; B41; 1.
DR	SMART; SM00194; PTPC; 1.
DR	PROSITE; PS00660; FERM_1; 1.
DR	PROSITE; PS00661; FERM_2; 1.
DR	PROSITE; PS00657; FERM_3; 1.
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR	PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
DR	PROSITE; PS00656; TYR_PHOSPHATASE_2; 1.
KW	Structural protein; Cytoskeleton; Hydrolase.
FT	DOMAIN 21 306 FERM.
FT	DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT	ACT_SITE 1121 1121 PHOSPHOCYCSTEINE INTERMEDIATE
FT	(BY SIMILARITY).
FT	DOMAIN 566 573 POLY-PRO.
FT	DOMAIN 709 716 POLY-GLU.
SQ	SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;
Query Match 22.4%; Score 477.5; DB 1; Length 1187;	
Best Local Similarity 29.6%; Pred. No. 2.7e-25;	
Matches 144; Conservative 67; Mismatches 152; Indels 123; Gaps 15;	
QY	14 DNDSEEGNSGMLNRSLPSSSQKMTPTKPIGNQNSENKVPSSHLSFSDKYELVYPEP 73 ::   ::
Db	709 ESESEE-----EEAPESVPQIPMLRKERMEYSQAQLAALARIPNKPPEYPGP 755
QY	74 LESDTDTWDVDSDRLRNKMSMDSETA-----GPSKTVS-----PVLSGSS---R 117 ::   ::
Db	756 RKS-----VSGALRDQASLPAPMARVLKHGPAKAISMSRTDPPAVNGASLGPS 807
QY	118 LSKDITETSVSEK-----ELTOL-----AQIRPLIF 142 ::   ::
Db	808 ISEPDLTSVKERVKEBPVKERPVSSEMFLEDSIIEREMMI RNLEKQKWAGLEAKQRFLML 867
QY	143 NS-----SARSARDCLNTLOXK-BELDIIIEFLEIQMTLPDDFNS 193 : :     ::
Db	868 AALNGLSVARVSGREENRVDA TRVPDMRFPTKKKGEEGMVFTEYEQIKPKANGIFST 927
QY	184 GNTLQNKDKRYDILPYDSTVRPL----GKNKDYNASYIRI VNHDEEFYFIATQGPLP 239 : :     ::
Db	928 AALPENAESRIEVVPYENRVELIPTYKENNTGYINDASHLVVVVGAEWHYIATQGPLP 987
QY	240 ETIEDFMQWLNNCMNVAMITREIECGVIKCYSWPISLKBPLEFBHFVSFVLETHVTQT 299 : :     ::
Db	988 HTCHDFQMWTQEOGVNVIA MVTAEEGGRTKSHRWY-----KLGSKHSSATYCKTKFVTT 1042
QY	300 YFTRVRPQIVKKST-----GKSCQVHLQFTKPDHCPTPASADFFIKY-----VR 344 : :     ::
Db	1043 KF--RTDSVCYATIGLKVHLLSGGERTVWHLYQTDMPDHCCPEDVOGFUSYLEETQSVR 1100
QY	345 YVRKSHITG-----ELLVHCAGVGRGTGVICVDVWFPSALEKKNYSFDINNI VTQMKQR 398 : :     ::
Db	1101 RHTNSMLEGTKNRHNP IIVHCSAGVGRGTGVLI LSLEMIYCLEHNKVEKVPVPMILLREQR 1160
QY	399 CGHIQT 404 
Db	1161 MFMIQT 1166 



RL Biochem. Biophys. Res. Commun. 203:479-484(1994).  
 CC -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and  
 CC non-hematopoietic origins.  
 CC -!- SIMILARITY: Contains 1 FERM domain.  
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D11842; BAA06628.1; --  
 CC PIR: JC2366; JC2366.  
 CC HSSP: Q06124; 2SHF.  
 CC MGD: MGI:102467; Ptpn14.  
 CC InterPro: IPR000299; Band 4.1.  
 CC InterPro: IPR000387; TYR Phosphatase.  
 CC InterPro: IPR000242; Tyr Pp.  
 CC Pfam: PF00373; Band 4.1; 1.  
 CC Pfam: PF00102; Y-phosphatase; 1.  
 CC PRINTS: PR00935; BAND41.  
 CC PRINTS: PR00700; PTPPHPTASE.  
 CC SMART: SM00295; B41; 1.  
 CC SMART: SM00194; PTPC; 1.  
 CC PROSITE: PS00660; FERM\_1; 1.  
 CC PROSITE: PS00661; FERM\_2; 1.  
 CC PROSITE: PS00657; FERM\_3; 1.  
 CC PROSITE: PS00383; TYR PHOSPHATASE 1; 1.  
 CC PROSITE: PS00055; TYR PHOSPHATASE PTP; 1.  
 CC PROSITE: PS00056; TYR PHOSPHATASE 2; 1.  
 CC Structural protein; Cytoskeleton; Hydrolase.  
 CC  
 CC FT DOMAIN 21 306 FERM.  
 CC FT DOMAIN 935 1189 PROTEIN-TYROSINE PHOSPHATASE.  
 CC FT ACT\_SITE 1123 1123 PHOSPHOCYSTEINE INTERMEDIATE  
 CC (BY SIMILARITY).  
 CC  
 CC FT DOMAIN 566 573 POLY-PRO.  
 CC FT DOMAIN 635 639 POLY-GLY.  
 CC FT DOMAIN 712 718 POLY-GLU.  
 CC SEQUENCE 1189 AA; 135030 MW; 2885B5F9C723303 CRC64;  
 CC  
 CC Query Match 21.4%; Score 456; DB 1; Length 1189;  
 CC Best Local Similarity 26.5%; Pred. No. 8.2e-24;  
 CC Matches 146; Conservative 73; Mismatches 149; Indels 182; Gaps 18;  
 CC  
 CC 20 CNGSNMLR-----NSLPSSQKMT-----PTKDFGNKMSNVK 55  
 CC 636 GGGGVNKRHSLEWNSWVRGMEANTLKSLNTPMAERNTLRQGSSEETGGVHG--L 692  
 CC 56 PSHH--LSPSKYELVYPELESOTHTWVDSDR-----SLNRNWSM 97  
 CC 693 PLYHKKTFSQATMLIHS--ESEEETLEAPQVPLVREKVEYSQAQLAARIPNP 750  
 CC 98 DSETAGSKTVSPVLSSGSSLSKDT-----123  
 CC 751 PPEYEGRXSVS---NGALQDQGTPLPAMARCVLRHGSPKALSVAELVNGASLG 807  
 CC 124 TSVSEKLTQI-----AQRPL 140  
 CC 808 PSISEPQTSVKERVKPEKVPKSPVSMFSLSDSIHEREMINLEKQMTGPOAQRPL 867  
 CC 141 IF-----NSSARMSDCLNTLQKKEELDIREFLEQMTLPDD-- 180  
 CC 868 MLAALNGLSVARVSGREDGRDATVPIDRLALKKLEDGMV--PTEYEQ--IPNKA 923  
 CC 181 ---FNSGNTLQNRKRYRDLIDYSTRPL-----GKQKDYINASYIRIYHSEYFIA 233

## RESULT 5

PTFV\_HUMAN  
 ID PTFV\_HUMAN STANDARD; PRT; 1337 AA.  
 AC Q12913; Q15255; Q8NEM2;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)  
 DE (HPTP eta) (protein-tyrosine phosphatase receptor type J) (Density  
 enhanced phosphatase-1) (DEP-1) (CD148 antigen).  
 GN PTPRJ OR DEPI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95024024; PubMed=7937872;  
 RA Cestman A., Yang Q., Tonks N.K.;  
 RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,  
 RT is enhanced with increasing cell density."  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95086212; PubMed=7994032;  
 RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;  
 RT "Molecular cloning, characterization, and chromosomal localization of  
 RT a novel protein-tyrosine phosphatase, HPTP eta."  
 RL Blood 84:4186-4194(1994).  
 RN [3]  
 RP SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER CYS-214 AND  
 RP PRO-276.  
 RC TISSUE=Colon;  
 RX MEDLINE=22084388; PubMed=12089527;  
 RA Ruitenkamp C.A.L., van Mezel T., Zanon C., Stassen A.P.M., Vilek C.,  
 RA Ceikos I., Kious A.M., Tripodis N., Perrakis A., Boerrigter L.,  
 RA Groot P.C., Lindeman J., Mooi W.J., Meijer G.A., Schooten G.,  
 RA Dauwerse H., Paces V., van Zandwijk N., van Ommen G.J.B., Denant P.;  
 RT "Ptprij is a candidate for the mouse colon-cancer susceptibility locus  
 RT Sccl and is frequently deleted in human cancers."  
 RL Nat. Genet. 31:295-300(2002).  
 CC -!- FUNCTION: May contribute to the mechanism of contact inhibition of  
 CC cell growth.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- PTM: N- and O-glycosylated.  
 CC -!- DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and  
 CC breast.  
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC -!- SIMILARITY: Contains 5 fibronectin type III domains.  
 CC -!- DATABASE: NAME=PTP; NOTE=CD guide CD148 entry.  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd148.htm".









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```
C C -----
C EMBL; D37801; BAA07053.1; -.
R R PIR; I58345; I58345.
R R HSSP; P29350; IGMZ.
R R MGI; MGI1134406; Ptpn21.
R R InterPro; IPR000299; Band 4.1.
R R InterPro; IPR000387; TYR_phosphatase.
R R Pfam; PF00373; Band 4.1.
R R Pfam; PF00373; Band 4.1.
R R PRINTS; PR00935; BAND41.
R R PRINTS; PR00700; PTPN21PHPTASE.
R R SMART; SW00295; B41; 1.
R R SMART; SW00194; PTEC; 1.
R R PROSITE; PS00660; FERM 1; 1.
R R PROSITE; PS00661; FERM 2; 1.
R R PROSITE; PS00057; FERM 3; 1.
R R PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
R R PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
R R PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
R R Structural protein; Cytoskeleton; Hydrolase.
T T DOMAIN 23 308
T T ACT_SITE 923 1176
T T DOMAIN 340 343
T T DOMAIN 565 572
T T SEQUENCE 1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;

Query Match 21.1%; Score 449; DB 1; Length 1176;
Best Local Similarity 28.5%; Pred. No. 2.5e-23;
Matches 138; Conservative 68; Mismatches 149; Indels 130; Gaps 16;

Y 44 IEGKNNSENKVP-----SHLSFSDKYELV-----YPEPLESDT--DETVMVSDRSLR 91
b 677 VESDKMQECTBEQGGYRSHKSLSDATMLDSDSEDEDELEDSRQQAISAVSEPRLT 736
Y 92 NKNW-----SMDSETAGP-----SKTVSPV--LSGSSRLSKD--TET 124
b 737 AAFSQELNVPASATPITGLHIFEPKPHVTEPEKRAKDIPVHLVTHPRDGLLTP 796
Y 125 SVSEKELTQAQI-----RPLFNSSARSAMRDCINTL--OKKEPDIIR----- 167
b 797 SNSESDLTSGRYARRDSVKRPVSDLLSGKKSVAEGLPLPGMKKTRDAKKIGPLK 856
Y 168 ---EFLEQNTLPDDFNSGNTL----- 187
b 857 AALNGLSRLFLPDEGKEVSTRAINDERCKVLEQRLEQGMVFTSYERILKRLVDSGCS 916
Y 188 -----QNRDKNRYDILPYDSTRVPLGKNKD----YINASYIRIVNHEEYFYIATQGPL 238
b 917 TARTLPENASERNFQDVLPPYDASVELVPTKENNTGYINASHIKVSVSGIENDYIATQGPL 976
Y 239 PETIEDFMQWLENNCNVNMTREIECVIKCYWPISLKEPFEHFSVFLETHVT 298
b 977 QNTCODFMQWVEQGVAIAMVTASEEGREKSPRIYP-----RLGSRHNTVTVGRFKIT 1031
Y 299 QYF-----TVRFVQIVKSTGKSCQVKHLQFTKWPDPHGTTPASADRFIKYRVYR--- 347
b 1032 TRPRTDSGCVATTGLKKHLLTGQERTVWHLQYTDWPEKGPEDLKGFLSVLEIQSVR 1091
Y 348 -----KSHITGPLLLHCHSAGVGTGTFVICVQVFFSAIKENVSFDMINTVTVQKQRC 399
b 1092 HTNSTSEPKSH-NPPLLHCHSAGVGTGTVILSEIHWACLEHNEVLIDIPRVLDMLRQORM 1150
Y 400 GMTQT 404
b 1151 MLVQT 1155
```

RESULT 9  
TN4\_HUMAN

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ID AC PTN4_HUMAN STANDARD; PRT; 926 AA.
DT DT P29074;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DE Protein tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48)
DE DE (Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG1)
GN GN PTPN4.
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX OX NCBI_TaxID=9606;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=91288564; PubMed=1648233;
RA RA Gu M., York J.D., Warshawsky I., Majerus P.W.;
RT RT "Identification, cloning, and expression of a cytosolic megakaryocyte
RT RT protein-tyrosine-phosphatase with sequence homology to cytoskeletal
RT RT Protein 4.1.";
RL RL Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871(1991).
RP RP [2]
RP RP SEQUENCE FROM N.A.
RX RX TISSUE=Colon;
RA RA MEDLINE=22388257; PubMed=12477932;
RA RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA RA Vallalao D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA RA Buttsfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT RT "Generation and initial analysis of more than 15,000 full-length
RT RT human and mouse cDNA sequences.";
RL RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC CC -I- FUNCTION: May act at junctions between the membrane and the
CC CC cytoskeleton.
CC CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC CC tyrosine + phosphate.
CC CC -I- SIMILARITY: Contains 1 PDM/DRH domain.
CC CC -I- SIMILARITY: Contains 1 PDZ/DRH domain.
CC CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC CC Non-receptor class subfamily.
CC CC -----
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CC CC -----
CC CC EMBL; M68941; AAA36530.1; -.
CC CC EMBL; BC010674; AAH10674.1; -.
CC CC F01; A41105; A41105.
CC CC HSSP; P29350; IGMZ.
CC CC Genew; HGNC:9656; PTPN4.
CC CC MIM; 176878; -.
CC CC GO; GO:0005737; Cytoplasm; TAS.
CC CC GO; GO:0004726; P:non-membrane spanning protein tyrosine phosph. .; TAS.
CC CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC CC InterPro; IPR000299; Band 4.1.
CC CC InterPro; IPR001478; PDZ.
CC CC InterPro; IPR000387; TYR_phosphatase.
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DR InterPro: IPR000242; Tyr_PP.  
DR Pfam: PF00373; Band_41; 1.  
DR Pfam: PF00595; PDZ; 1.  
DR Pfam: PF0102; Y_phosphatase; 1.  
DR PRINTS: PR00935; BAND41.  
DR PRINTS: PR00700; PRTYPHPHASE.  
DR SMART: SM00295; B41; 1.  
DR SMART: SM00228; PDZ; 1.  
DR SMART: SM00194; PTPC; 1.  
DR PROSITE: PS00660; FERM_1; 1.  
DR PROSITE: PS00661; FERM_2; 1.  
DR PROSITE: PS00557; FERM_3; 1.  
DR PROSITE: PS0106; PDZ; 1.  
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.  
DR PROSITE: PS00384; TYR_PHOSPHATASE_2; 1.  
DR PROSITE: PS00556; TYR_PHOSPHATASE; 1.  
DR PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 1.  
KW Structural protein; Cytoskeleton; Hydrolase.  
FT DOMAIN 29 312 FERM.  
FT DOMAIN 517 589 PDZ.  
FT DOMAIN 677 926 PROTEIN-TYROSINE PHOSPHATASE.  
FT ACT_SITE 852 PHOSPHOCYSTEINE INTERMEDIATE  
FT ACT_SITE 852 (BY SIMILARITY).  
FT SEQUENCE 926 AA; 105911 MW; 4DAC6A87A675CFB0 CRC64;  
Query Match 20.9%; Score 446.5; DB 1; Length 926;  
Best Local Similarity 27.6%; Pred. No. 2.7e-23;  
Matches 121; Conservative 63; Mismatches 166; Indels 89; Gaps 9;  
QY 24 NLNRLNSLSSQKMTPTKPIFGNKNNSNKKVSHLSFSDKYLVLVPEPLESDTETVW 83  
DB 490 HINETDIPSSPEKPTGGIGDHNLVLRMKPDNGRFGNKGVDQKQKPVIVSRVA- 548  
QY 84 DVSDRLNRNWSMDETAGPKNTVSPVLSSGSRSLSKDTSTSVSEKLTQLAQIRPLIFN 143  
DB 549 -----PCTPADLCVPRLNQEGDQVVLINGRDIAETHDQVV-----LFIK 587  
QY 144 SSARSAMRCLNTLQKEELDIIREFLE-----QMTLP 178  
DB 588 ASCERHSGELMLLVRENAVYDVVEKLENEPDPQYIPEKAPLDSVHODHSILRESMIQLA 647  
QY 179 DDNSGNLT-----QNRDNRYRDLIPDSTVPLGKNDYNA 217  
DB 648 EGLITGVLTQFQLYRKRPGMTSCAKLPQNSKNRYRDISPYATRVILKGNEDYNA 707  
QY 218 SYIR-----IVNBEERYFIATQPLPETIEDFMQVLENNCNVIAITREISGVIK 270  
DB 708 NYINMEIPSSIIHQ-----YIACQGPLHTCTDFQMTWEQSSVMVWLTQVGRGVK 762  
QY 271 CYSYWPISLKEPLEPFPVPLETFHTVQYFVTRVQ-----IVKKGTSQCVKHLQFTKW 327  
DB 763 CQYWP-----EPTGSSSYCYQVTCSEGNATYIPRMTLFPQBNKNSRPLTQIQYIAW 818  
QY 328 PDHGTPTASADFFLYVYVRKSHI--TGPLLVHCSAGVGRGTGVFCVDVVFSAIEKNYSF 385  
DB 819 PDHGVDPSSDFLDFVCHVRNKGAGKEEPVHVHCSAGIGRTGLVLTMETAMCLIECNQPV 878  
QY 386 DIMNIVTQMKQKQCGMIQT 404  
DB 879 YPLDIVRTWRDQRMNIQT 897  
RESULT 10  
PTNS_HUMAN STANDARD; PRT; 1948 AA.  
AC Q13332; Q15718; Q16341;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)  
DE (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).  
GN PTPRS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=96102179; PubMed=8524829;  
RA Pulido R., Serra-Pages C., Tang M., Streuli M.;  
RT "The LAR/pnp delta/ptp sigma subfamily of transmembrane protein-  
RT tyrosine-phosphatases: multiple human LAR, PTP delta, and ptp sigma  
RT isoforms are expressed in a tissue-specific manner and associate with  
RT the LAR-interacting protein Lip.1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96255038; PubMed=8992885;  
RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;  
RT "Human protein tyrosine phosphatase-sigma: alternative splicing and  
RT inhibition by bisphosphonates.";  
RL J. Bone Miner. Res. 11:535-543(1996).  
RN [3]  
RP SEQUENCE OF 1-126 FROM N.A.  
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J., Liu S.,  
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,  
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
RA Olsen A.S., Carrano A.V.;  
RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1503-1589 FROM N.A.  
RX MEDLINE=92119637; PubMed=1370651;  
RA Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,  
RA Isai K., Yachi A.;  
RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";  
RL Cancer Res. 52:737-740(1992).  
CC -!- FUNCTION: Interacts with LAR-interacting protein LIP.1.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2O) = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=5;  
CC Comment=Additional isoforms seem to exist;  
CC Name=PTPS;  
CC IsoId=Q13332-1; Sequence=Displayed;  
CC Name=PTPS-MEA;  
CC IsoId=Q13332-2; Sequence=VSP_050021;  
CC Name=PTPS-MEB;  
CC IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;  
CC Name=PTPS-MEC;  
CC IsoId=Q13332-4; Sequence=VSP_050024;  
CC Name=PTPS-F4;  
CC IsoId=Q13332-5; Sequence=VSP_050023, VSP_050025;  
CC -!- TISSUE SPECIFICITY: Detected in all tissues tested except for  
CC placenta and liver.  
CC -!- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE  
CC PHOSPHATASE FAMILY.  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 8 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC -----  
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CC or send an email to license@sib-sib.ch).  
CC -----  
DR EMBL: U35234; AAC50299.1; -.  
DR EMBL: U40317; AAC50567.1; -.  
DR
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DR EMBL; AC005790; AAC2892.1; -.
DR EMBL; S78080; AA221146.2; -.
DR HSP; P18052; 1YFO.
DR Genew; HGNC:9681; PTPRS.
DR MIM; 601576; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005001; F: transmembrane receptor protein tyrosine pho. .; TAS.
DR InterPro; IPR009597; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FN_III subd.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR00387; Tyr_phosphatase.
DR InterPro; IPR00242; Tyr_PP.
DR Pfam; PF00041; fn3; 8.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; ENTPBIII.
DR PRINTS; PR00700; PTPRHPTASE.
DR SMART; SM00060; FN3; 7.
DR SMART; SM00408; IGc2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS00556; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00556; TYR_PHOSPHATASE 2; 2.
DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
DR Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
DR SIGNAL 1 29
DR CHAIN 30 1948
DOMAIN 30 1282
TRANSMEM 1283 1303
DOMAIN 1304 1948
DOMAIN 33 123
DOMAIN 135 233
DOMAIN 245 327
DOMAIN 329 423
DOMAIN 426 522
DOMAIN 525 615
DOMAIN 618 717
DOMAIN 720 831
DOMAIN 834 926
DOMAIN 928 1031
DOMAIN 1036 1151
DOMAIN 1393 1648
DOMAIN 1680 1930
DOMAIN 641 644
DISULFID 54 107
DISULFID 156 216
ACT_SITE 266 311
ACT_SITE 1589 1589
ACT_SITE 1880 1880
CARBOHYD 263 263
CARBOHYD 308 308
CARBOHYD 733 733
CARBOHYD 940 940
VARSPPLIC 190 198
VARSPPLIC 236 239
VARSPPLIC 617 1034
VARSPPLIC 784 792
VARSPPLIC 1035 1035
VARSPPLIC 1350 1365
VARSPPLIC 1366 1366

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EMBL; AC005790; AAC2892.1; -.  
EMBL; S78080; AA221146.2; -.  
HSP; P18052; 1YFO.  
Genew; HGNC:9681; PTPRS.  
MIM; 601576; -.  
GO; GO:0005887; C: integral to plasma membrane; TAS.  
GO; GO:0005001; F: transmembrane receptor protein tyrosine pho. .; TAS.  
InterPro; IPR009597; FN\_III-like.  
InterPro; IPR003961; FN\_III.  
InterPro; IPR003962; FN\_III subd.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003598; IG\_c2.  
InterPro; IPR00387; Tyr\_phosphatase.  
InterPro; IPR00242; Tyr\_PP.  
Pfam; PF00041; fn3; 8.  
Pfam; PF00047; ig; 3.  
Pfam; PF00102; Y\_phosphatase; 2.  
PRINTS; PR00014; ENTPBIII.  
PRINTS; PR00700; PTPRHPTASE.  
SMART; SM00060; FN3; 7.  
SMART; SM00408; IGc2; 3.  
SMART; SM00194; PTPC; 2.  
PROSITE; PS00835; IG\_LIKE; 3.  
PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
PROSITE; PS00383; TYR\_PHOSPHATASE 2; 2.  
PROSITE; PS00556; TYR\_PHOSPHATASE 1; 2.  
PROSITE; PS00556; TYR\_PHOSPHATASE 2; 2.  
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
SIGNAL 1 29  
CHAIN 30 1948  
DOMAIN 30 1282  
TRANSMEM 1283 1303  
DOMAIN 1304 1948  
DOMAIN 33 123  
DOMAIN 135 233  
DOMAIN 245 327  
DOMAIN 329 423  
DOMAIN 426 522  
DOMAIN 525 615  
DOMAIN 618 717  
DOMAIN 720 831  
DOMAIN 834 926  
DOMAIN 928 1031  
DOMAIN 1036 1151  
DOMAIN 1393 1648  
DOMAIN 1680 1930  
DOMAIN 641 644  
DISULFID 54 107  
DISULFID 156 216  
ACT\_SITE 266 311  
ACT\_SITE 1589 1589  
ACT\_SITE 1880 1880  
CARBOHYD 263 263  
CARBOHYD 308 308  
CARBOHYD 733 733  
CARBOHYD 940 940  
VARSPPLIC 190 198  
VARSPPLIC 236 239  
VARSPPLIC 617 1034  
VARSPPLIC 784 792  
VARSPPLIC 1035 1035  
VARSPPLIC 1350 1365  
VARSPPLIC 1366 1366





CC EMBL; AF152556; AAD34158.4; -  
DR EMBL; AY026861; AAK18741.1; -  
DR EMBL; AY026862; AAK18742.1; -  
DR EMBL; AY026863; AAK18743.1; -  
DR EMBL; AF244125; AAF44712.1; -  
DR EMBL; AF162856; AAF82400.2; -  
DR EMBL; AF162857; AAF82401.1; -  
DR HSP; P28827; 1RPM.  
DR MGD; MGI:1321152; Ptdrc.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR000998; MAM\_domain.  
DR InterPro; IPR003595; PTPC\_motif.  
DR InterPro; IPR00387; Tyr\_phosphatase.  
DR InterPro; IPR00242; Tyr\_PP.  
DR Pfam; PF00041; In3; 3.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF0102; Y\_phosphatase; 2.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR PRINTS; PR00700; PTPC motif.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTPC; 2.  
DR SMART; SM00404; PTPC motif; 2.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00740; MAM; 1.  
DR PROSITE; PS00600; MAM; 2; 1.  
DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
DR PROSITE; PS0056; TYR PHOSPHATASE 2; 2.  
DR PROSITE; PS0055; TYR PHOSPHATASE\_PTP; 2.  
DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
KW Immunoglobulin domain; Repeat; Alternative splicing.  
FT SIGNAL 1 29  
FT CHAIN 30 1454  
FT FT 30 770  
FT DOMAIN 771 791  
FT TRANSMEM 792 1454  
FT DOMAIN 134 195  
FT DOMAIN 197 288  
FT DOMAIN 293 378  
FT DOMAIN 390 484  
FT DOMAIN 485 588  
FT DOMAIN 593 731  
FT DOMAIN 902 1156  
FT DOMAIN 1188 1450  
FT ACT\_SITE 1097 1097  
FT FT 1391 1391  
FT ACT\_SITE 217 271  
FT DISULFID 82 82  
FT CARBOHYD 102 102  
FT CARBOHYD 141 141  
FT CARBOHYD 212 212  
FT CARBOHYD 425 425  
FT CARBOHYD 514 514  
FT CARBOHYD 551 551  
FT CARBOHYD 605 605  
FT CARBOHYD 658 658  
FT CARBOHYD 688 688  
FT VARSPPLIC 731 749  
FT FT 794 794  
FT VARSPPLIC 794 794  
FT VARSPPLIC 1007 1007  
FT VARSPPLIC 1007 1007  
FT FT 13 16  
FT CONFLICT

FT CONFLICT 21 21  
FT CONFLICT 34 37  
FT CONFLICT 87 87  
FT CONFLICT 254 254  
FT CONFLICT 266 266  
FT CONFLICT 602 602  
FT CONFLICT 822 822  
FT CONFLICT 825 825  
FT CONFLICT 844 845  
FT CONFLICT 1016 1016  
FT CONFLICT 1049 1049  
FT CONFLICT 1050 1050  
FT CONFLICT 1076 1076  
FT CONFLICT 1103 1103  
FT CONFLICT 1259 1259  
FT CONFLICT 1266 1266  
FT CONFLICT 1269 1269  
SQ SEQUENCE 1454 AA; 163012 MW; C60464F7B423F8A8 CRC64;  
Query Match 20.7%; Score 442.5; DB 1; Length 1454;  
Best Local Similarity 27.9%; Pred. No. 9.2e-23;  
Matches 131; Conservative 62; Mismatches 157; Indels 119; Gaps 16;  
QY 15 NDEEGNSGNLNLNSLPSSSQKMTPTKPI-----FGKMNSENVKPSHLSPSDKYELVY 70  
Db 716 NGETKINCVRATKGA-PMGSAQVTPGTPLCLLTASTQNSNTPV----- 760  
QY 71 PEPLESDTDTV-----WDVSDRSLRNWNMSMDSETAGSKTVSP 110  
Db 761 -----EKQVNTVMAGVIAGLLMFIILLGVMLTIKRRKLAKKQKQTS---GAQREMGP 813  
QY 111 VLS-----GSRLLSKDTE--TSVSEKELTOLA----- 135  
Db 814 VASTDKPTAKLTNRNDEGFSSSQDVGFTGDSRGELSQFTLTIOHPYNTCDPVMSY 873  
QY 136 ---QIRPLIFNSSARSAMDCLNTLOK-----KEELDIREFLELEQMTLPDDFNS 183  
Db 874 PRDQPPAI-----RVADLLQHTQKRCQGGPKKEEYALPEGQTASNDTAKED--- 923  
QY 184 GNTLQNRDNRYRDLIPYDSTRVPL-----GKNQDYINASYIRVNHBEYFYIATQGPL 238  
Db 924 ---ENRNKNRYGNIISYDHSRVELLVLDGPHSDYINANYID--GYRPHRYIATQGP 977  
QY 239 PTTIEDFQWLENNCNVIMITREIECGVTKCVSYMPISLKEPLBEPHPSVFLETHVT 298  
Db 978 QETVDFWRNMQENSASIVMTNLVEGRVKCVRYMPDDTETVGDIX--VLTIEPLA 1035  
QY 299 QYFTVRVQIVKSKGQCVKHLQFTKWPDPHGTFPASADPFIKYRVYR--KSHITGPLL 356  
Db 1036 EY-VIRTTVQKKGVEIRLRLPHFTSMPDHGVPCVATGLLGFVRQVKFLNPPAEP 1094  
QY 357 VHCASGAGRTGVCIVDVVFSIAEKNSYFDIMNIVTQMKORCGMIOTK 405  
Db 1095 VHCASGAGRTGCFIAIDTMDWAENEGYVDIFNCVRELRAQRVNLVQTE 1143  
RESULT 14  
ID PTPT HUMAN STANDARD; PRT; 1463 AA.  
AC O14522; O43655; O75664; Q9BR24; Q9H0Y8; Q9NTLL; Q9NU72;  
AC Q9UBD2; Q9JUL7;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase T precursor (BC 3.1.3.48)  
DE (R-PTP-T) (R-PTP-tho).  
GN PTPPT OR KIAA0283.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.

RX MEDLINE=98267260; PubMed=9602027;  
 RA McAndrew P.E., Frostholt A., White R.A., Rotter A., Burghes A.H.M.;  
 RT "Identification and characterization of RPTP who, a novel RPTP  
 RT mu/kappa-like receptor protein tyrosine phosphatase whose expression  
 RL is restricted to the central nervous system.";  
 RV Brain Res. Mol. Brain Res. 56:9-21(1998).  
 RP [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=97323006; PubMed=9179496;  
 RA Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M.,  
 RA Seki N., Nomura N.;  
 RT "Construction and characterization of human brain cDNA libraries  
 RT suitable for analysis of cDNA clones encoding relatively large  
 RT proteins.";  
 RL DNA Res. 4:53-59(1997).  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.B., Collier R.S., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graiham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leheslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showken R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RP [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=22730707; PubMed=11423001;  
 RA Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;  
 RT "Genomic organization and alternative splicing of the human and mouse  
 RT RPTpho genes.";  
 RL BMC Genomics 2:1-1(2001).  
 RP [5]  
 RP ERRATUM.  
 RX MEDLINE=22730717; PubMed=11814386;  
 RA Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;  
 RL BMC Genomics 2:5-5(2001).  
 RP [6]  
 RP FUNCTION: May be involved in both signal transduction and cellular  
 RP adhesion in the CNS.  
 RP CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 RP tyrosine + phosphate.  
 RP SUBCELLULAR LOCATION: Type I membrane protein.  
 RP ALTERNATIVE PRODUCTS:  
 RP Event=Alternative splicing; Named isoforms=2;  
 RP Name=1;  
 RP IsoId=O14522-1; Sequence=Displayed;  
 RP Name=2;  
 RP IsoId=O14522-2; Sequence=VSP\_007802;  
 RP TISSUE SPECIFICITY: Expression is restricted to the CNS.  
 RP SIMILARITY: Contains 1 MAM domain.  
 RP SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 RP SIMILARITY: Contains 4 fibronectin type III domains.

CC CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AF043644; AAD09421.2; -  
 CC EMBL; AB006621; BAA22952.2; ALT\_INIT.  
 CC EMBL; AL021395; CAC24740.2; -  
 CC EMBL; AL022239; CAC26785.1; -  
 CC EMBL; AL024473; CAA19686.1; -  
 CC EMBL; AL031656; CAB51752.1; -  
 CC EMBL; AL049812; CAB52429.1; -  
 CC EMBL; AL121763; CAC21701.1; -  
 CC EMBL; AL136461; CAB91828.1; -  
 CC EMBL; Z93942; CAC26841.1; -  
 CC HSPF; P28827; IRPM  
 CC Genew; HGNC:5682; PTPRT.  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.  
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.  
 CC InterPro; IPR003961; FN III.  
 CC InterPro; IPR007110; Ig-like  
 CC InterPro; IPR000998; MAM domain.  
 CC InterPro; IPR003595; PTPC motif.  
 CC InterPro; IPR000387; Tyr phosphatase.  
 CC InterPro; IPR000242; Tyr\_PP.  
 CC Pfam; PF00041; fn3; 3.  
 CC Pfam; PF00629; MAM; 1.  
 CC Pfam; PF00102; Y\_phosphatase; 2.  
 CC PRINTS; PR00020; MAMDOMAIN.  
 CC PRINTS; PR00700; PRTYPHPTASE.  
 CC SMART; SM00060; FN3; 3.  
 CC SMART; SM00137; MAM; 1.  
 CC SMART; SM00194; PTPC; 2.  
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 CC PROSITE; PS00740; MAM\_1; 1.  
 CC PROSITE; PS00600; MAM\_2; 1.  
 CC PROSITE; PS00383; TYR\_PHOSPHATASE\_2; 2.  
 CC PROSITE; PS00056; TYR\_PHOSPHATASE\_PTP; 2.  
 CC PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 CC Immunoglobulin domain; Repeat; Alternative splicing.  
 CC SIGNAL 1 25 POTENTIAL.  
 CC CHAIN 26 1463 RECEPTOR-TYPE PROTEIN-TYROSINE  
 CC DOMAIN 26 766 PHOSPHATASE T.  
 CC TRANSMEM 767 787 EXTRACELLULAR (POTENTIAL).  
 CC DOMAIN 788 1463 POTENTIAL.  
 CC DOMAIN 30 191 CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 193 284 MAM.  
 CC DOMAIN 289 374 IG-LIKE C2-TYPE.  
 CC DOMAIN 386 480 FIBRONECTIN TYPE-III 1.  
 CC DOMAIN 481 584 FIBRONECTIN TYPE-III 2.  
 CC DOMAIN 589 726 FIBRONECTIN TYPE-III 3.  
 CC DOMAIN 911 1165 FIBRONECTIN TYPE-III 4.  
 CC DOMAIN 1197 1459 PROTEIN-TYROSINE PHOSPHATASE 1.  
 CC ACT\_SITE 1106 1106 PROTEIN-TYROSINE PHOSPHATASE 2.  
 CC ACT\_SITE 1400 1400 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 CC SIMILARITY).  
 CC ACT\_SITE 1400 1400 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 CC SIMILARITY).  
 CC DISULFID 213 267 POTENTIAL.  
 CC CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).



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FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 684 684 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT VARSPLIC 726 744 Missing (in isoform 2).
FT CONFLICT 29 29 P -> A (IN REF. 3).
FT CONFLICT 60 60 T -> W (IN REF. 1).
FT CONFLICT 375 375 A -> P (IN REF. 1).
FT CONFLICT 801 803 MISSING (IN REF. 1).
FT CONFLICT 889 889 L -> P (IN REF. 1).
SQ SEQUENCE 1463 AA, 164275 MW, BE4B4R8B3E8A4017 CRC64;

Query Match 20.7%; Score 442; DB 1; Length 1463;
Best Local Similarity 28.0%; Pred. No. 1e-22;
Matches 131; Conservative 60; Mismatches 155; Indels 122; Gaps 16;

QY 25 LNLRLSPSSQKQVTPKPIF-----GNKNSENKVPKSHLSFSDKYELVYPELESYTD 79
Db 720 VRLATKAPMGSAQVTPGTPCLLTGASTQNSNTVEP-----EKQVD 761
QY 80 ETV-----WVSDSLRNKNSMDSRTAGPSK 106
Db 762 NTVKAGVIAGLFIILLGLVMTIKERNAYSYLSQRLAKKQKETQS---GAQR 818
QY 107 TVSPVLS-----GSSRLSKDTE--TSVSEKELTO---LAQIRPL----- 140
Db 819 EMGPVASADKFTTKLSARNDGFSFSSQDVNGFTDGRGELSQPTLTITQHPYRTCDPV 878
QY 141 -----IFNSARSARMDCLNTLQK-----KEELDIRLEFELEQMTLPDPFNSG 184
Db 879 EMSYPRDQFLAIRVA--DLLQHTQMGQGGYGFKEVEALPEQQTASNTAKED--- 932
QY 185 NTLQNDKNRYDILPDSYRVEI-----GKNQYINASYIVNHESEYFIATQPLP 239
Db 933 ---ENRNKRYGNTIISYDHSKRVLLVLDGPHSDYINANYID--GYHPRHYIATQGPQ 987
QY 240 ETIEDFMQVLENNCNVMIAMITREICGVKIKSVYWPISLKEPLFEFFSVFLSTFHTVQ 299
Db 988 ETVKDFRMVWQENSASIVMTNLVEVGRVKVRYWPDQTEVYGDIK--VTLIETEPLE 1045
QY 300 YFTRVFOIVKSGTKSQCKVHLQFTKWDHGTTPASADFIKYRYVR--KSHITGLLV 357
Db 1046 Y-VIRTFVQKKGHEIRLEIRLHFHTSWPDHGVPCVATGLGFRVQVFLNPPAGSIVV 1104
QY 358 HCSAGVGRGTGFIQVVDVVSFAIEKNYSFDMIVTQMRKQRCGMQTK 405
Db 1105 HCSAGAGRTGCFIAIDTMDLWASNEGWDIFNCVRELRAQRVNLVQTE 1152

RESULT 15
PTN2_HUMAN STANDARD; PRT; 415 AA.
AC P17706; Q96HR2;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE Protein-tyrosine phosphatase, non-receptor type 2 (EC 3.1.3.48) (T-
DE cell protein-tyrosine phosphatase) (TCPTP).
GN PTN2 OR PTP
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA MEDLINE=89315776; PubMed=2546150;
RA Cool D., Tonks N., Charbonneau H., Walsh K., Fischer E.H., Krebs E.G.;
RT "cDNA isolated from a human T-cell library encodes a member of the
RT protein-tyrosine-phosphatase family.";

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RL Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261(1989).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=92115688; PubMed=1731319;
RA Mosinger B. Jr., Tillmann U., Westphal H., Tremblay M.L.;
RA "Cloning and characterization of a mouse cDNA encoding a cytoplasmic
RT protein-tyrosine-phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992).
RN [3]
RX SEQUENCE FROM N.A. (ISOFORM PTP2).
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kattaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC -!- tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=PTP;
CC IsoId=P17706-1; Sequence=Displayed;
CC Name=PTPA;
CC IsoId=P17706-2; Sequence=VSP_005125;
CC -!- TISSUE SPECIFICITY: PTPA isoform is probably the major PTP
CC expressed in human tissues. PTPB isoform was found in T-cells and
CC in placenta.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M25393; AAA65997.1; --
CC EMBL; M81478; --; NOT ANNOTATED_CDS.
CC EMBL; BC008244; AAH08244.1; --
CC FDB; 118K; 28-AUG-02.
CC Genew; HGNC:9650; PTPN2.
CC MIM; 176887; --
CC GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; T-cell; Alternative splicing; 3D-structure.
DOMAIN 42 286 PROTEIN-TYROSINE PHOSPHATASE.

```



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 17:10:06 ; Search time 46 Seconds  
(without alignments)  
2777.932 Million cell updates/sec

Title: US-09-095-478A-7

Perfect score: 2133

Sequence: 1 MSPRKVRGKGRDNDDEEG.....DIMNIVTMRKQRCGMIOTK 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_rbc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	426	11	O55082 mus musculus
2	1231	57.7	398	4	O9V406 homo sapien
3	606	28.4	2460	11	O64512 mus musculus
4	599.5	28.1	2484	6	Q28006 bos taurus
5	468	21.9	292	4	Q8N4S3
6	463.5	21.7	926	11	Q9WU22
7	459	21.5	832	13	Q90947 gallus galli
8	457	21.4	1222	13	Q8MY44 eptaretus
9	456.5	21.4	758	11	Q7TNG1 mus musculus
10	456	21.4	1100	13	Q8MY45 eptaretus
11	456	21.4	1187	13	Q8MY42 eptaretus
12	456	21.4	1202	13	Q8MY43 eptaretus
13	454	21.3	1216	13	Q9IBD8 cyprinus ca
14	451.5	21.2	907	13	Q8MY41 eptaretus
15	451.5	21.2	1598	11	Q8CIW2 mus musculus
16	450	21.1	849	11	Q9JLJ8 mus musculus

17	449.5	21.1	1102	11	Q8QVW7
18	449	21.1	579	11	Q3JU07
19	448.5	21.0	2051	5	O44328
20	446	20.9	1238	11	Q8K3Q2
21	445.5	20.9	592	13	Q7SY37
22	445.5	20.9	615	13	Q9IAI8
23	445.5	20.9	1399	4	O75870
24	445	20.9	1024	4	Q8WX29
25	445	20.9	1406	13	Q9W6V5
26	444	20.8	1216	11	Q82884
27	443.5	20.8	1501	11	Q7TTL7
28	443	20.8	361	11	Q61373
29	442.5	20.7	468	13	Q9IBAO
30	442.5	20.7	498	5	Q8IRM6
31	442.5	20.7	578	5	Q9W324
32	442.5	20.7	797	5	Q8IRM7
33	442.5	20.7	827	5	Q9W323
34	442.5	20.7	857	13	Q90YJ4
35	441.5	20.7	353	4	Q96AU5
36	441	20.7	336	11	Q9QWQ7
37	441	20.7	2271	13	Q9I909
38	440.5	20.7	1501	11	Q9QWQ0
39	440.5	20.7	1883	11	Q64605
40	439.5	20.6	468	13	Q9IBAZ
41	439.5	20.6	1502	4	Q9UM81
42	439	20.6	1226	11	Q7TSY7
43	438	20.5	508	11	Q8OW11
44	438	20.5	649	11	Q64641
45	438	20.5	694	13	Q7ZYN2

## ALIGNMENTS

### RESULT 1

Q55082	PRELIMINARY;	PRT;	426 AA.
ID	O55082		
AC	O55082;		
DT	01-JUN-1998 (TRENBLREL. 06, Created)		
DT	01-JUN-1998 (TRENBLREL. 06, Last sequence update)		
DT	01-JUN-2003 (TRENBLREL. 24, Last annotation update)		
DE	Protein-tyrosine-phosphatase (EC 3.1.3.48).		
GN	PTN20.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RX	MEDLINE=98070510; PubMed=9407093;		
RA	Ohnishi M., Kuramochi S., Matsuda S., Yamamoto T.;		
RT	"Molecular cloning and characterization of a novel cytoplasmic		
RT	protein-tyrosine phosphatase that is specifically expressed in		
RT	spermatocytes.";		
RL	J. Biol. Chem. 272:33092-33099(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RL	60,770 full-length cDNAs."		
RL	Nature 420:563-573(2002).		
DR	EMBL; D64141; BAA23761.1; -		
DR	EMBL; AK029493; BAC26476.1; -		
DR	HSSP; Q06124; 2SHP.		
DR	MGI; MGI:1196295; Ptpn20.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0004727; P:phosphatase act. .; IEA.		
DR	GO; GO:0008470; P:protein amino acid dephosphorylation; IEA.		
DR	InterPro; IPR000387; Tyr_phosphatase.		

DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase.1.  
 DR PRINTS; PR00700; PRTVPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hypothetical protein; Hydrolyase.  
 DR KW NON\_TER 1  
 DR SO SEQUENCE 426 AA; 49118 MW; 2835FB1337950284 CRC64;  
 Query Match 100.0%; Score 2133; DB 11; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-159;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFPRKVRGKTQRDNDEBEGSGNINLNSLPSSQKMTPTKIPFGNKNSENKVPSSHL 60  
 DB 1 MSFPRKVRGKTQRDNDEBEGSGNINLNSLPSSQKMTPTKIPFGNKNSENKVPSSHL 60  
 QY 61 SFSDKYELVYPPLESDDTETVWDSRLNRNWSMDSETAGSKTVGVLGSGSRLSK 120  
 DB 61 SFSDKYELVYPPLESDDTETVWDSRLNRNWSMDSETAGSKTVGVLGSGSRLSK 120  
 QY 121 DTETSVSEKLTQIAQIRPLIFNSARSAMDCLNTLOKKELDIIRFLELEQMTLPDD 180  
 DB 121 DTETSVSEKLTQIAQIRPLIFNSARSAMDCLNTLOKKELDIIRFLELEQMTLPDD 180  
 QY 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIYNHHEEYFYIATQGLPE 240  
 DB 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIYNHHEEYFYIATQGLPE 240  
 QY 241 TTEDFWQVLENNCNVIAMITREIECGVICSVPISLKEPLEFHFVLETHVTOY 300  
 DB 241 TTEDFWQVLENNCNVIAMITREIECGVICSVPISLKEPLEFHFVLETHVTOY 300  
 QY 301 FTVRVQIVKSKGSCQVKHLQTKPDHGTTPASADFFPIKYVYVRKSHITGPLLVCES 360  
 DB 301 FTVRVQIVKSKGSCQVKHLQTKPDHGTTPASADFFPIKYVYVRKSHITGPLLVCES 360  
 QY 361 AGVGRTGVICVDVVFSAIEKNYSFDIMNIVTQNRKQRCGMIOTK 405  
 DB 361 AGVGRTGVICVDVVFSAIEKNYSFDIMNIVTQNRKQRCGMIOTK 405

## RESULT 2

QY406 ID Q9Y406 PRELIMINARY; PRT; 398 AA.  
 AC Q9Y406  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein (fragment).  
 DE DKFZF56K0524.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 XX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Ansoorge W., Winkler U., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AL050040; CAB43248.1; -  
 RL PIR; T08716; T08716.  
 RL HSSP; Q06124; 28HP.  
 RL GO; GO:0016787; F:hydrolyase activity; IEA.  
 RL GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 RL GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 RL InterPro; IPR000387; TYR\_phosphatase.  
 RL Pfam; PF00102; Y\_PP.  
 RL PRINTS; PR00700; PRTVPHPTASE.  
 RL SMART; SM00194; PTPC; 1.  
 RL PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hypothetical protein; Hydrolyase.  
 DR KW NON\_TER 1  
 DR SO SEQUENCE 398 AA; 45690 MW; 857AAD003747870A2 CRC64;  
 Query Match 57.7%; Score 1231; DB 4; Length 398;  
 Best Local Similarity 64.9%; Pred. No. 3.2e-88;  
 Matches 238; Conservative 46; Mismatches 75; Indels 8; Gaps 2;

QY 40 PTKPIFGKNKSENKVPSSHLSPFSDKYELVYPPLESDDTETVWDSRLNRNWSMD 99  
 DB 18 PQQVQVFNKVNKSKVLSLRNPHNDYEDVEFESGSDPSMTARGPFRDRWSSEDE 77  
 QY 100 ETAGPSKTVSPVLGSSRLSKDTSTSEKELTQIAQIRPLIFNSARSAMDCLNTLOK 159  
 DB 78 EAAGPSQALSPILLS-----DTRKIVSEGLDQIAQIRPLIFNFHEQTAQKCLILEE 130  
 QY 160 K-EELDIIRFLELEQMTLPDDNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDYINAS 218  
 DB 131 KYAADIWQEFMALEKRLNLPGEFYSGQPSNREKRYRDLIPYDSTRVPLGSKDYINAS 190  
 QY 219 YIRIYNHHEEYFYIATQGLPETIEDFWQVLENNCNVIAMITREIECGVICSVPIS 278  
 DB 191 YIRIYNHHEEYFYIATQGLPETIEDFWQVLENNCNVIAMITREIECGVICSVPIS 250  
 QY 279 LKEPLEFHFVLETHVTOYFTVRVQIVKSKGSCQVKHLQTKPDHGTTPASADFF 338  
 DB 251 LKKPLELKHFRVLENTQILQYFIIRNFQVVEKSTGTSVSKQLQTKPDHGTTPASADS 310  
 QY 339 PIKYVYVRKSHITGPLLVCESAGVGRTGVICVDVVFSAIEKNYSFDIMNIVTQNRKOR 398  
 DB 311 PIKYVYVRKSHITGPLLVCESAGVGRTGVICVDVVFSAIEKNYSFDIMNIVTQNRKOR 370  
 QY 399 CGMIQTK 405  
 DB 371 SCWVQTK 377

## RESULT 3

Q64512 ID Q64512 PRELIMINARY; PRT; 2460 AA.  
 AC Q64512; Q62135; Q61494; Q64499;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Protein-tyrosine phosphatase, NONRECEPTOR-type, 13 (EC 3.1.3.48)  
 DE (protein-tyrosine phosphatase Rip) (Phosphoprotein phosphatase)  
 DE (protein-tyrosine-phosphatase) (Phosphotyrosine phosphatase) (PTPase)  
 DE (PTP36).  
 GN PTPN13 OR PTP14.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 XX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=SKIN;  
 RC MEDLINE=96340953; PubMed=8749712;  
 RA Hendriks W., Schepens J., Baechner D., Rijss J., Zeeuwen P.,  
 RA Zechner U., Hameister H., Wieringa B.,  
 RT "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase  
 RT with similarities to submembranous proteins".  
 RL J. Cell. Biochem. 59:418-430(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DBA/2;  
 RC MEDLINE=95145716; PubMed=7843407;  
 RA Chida D., Kume T., Mukoyama Y., Tabata S., Nomura N., Thomas M.,  
 RA Watanabe T., Oishi M.,  
 RT "Characterization of a protein tyrosine phosphatase (Rip) expressed at  
 RT a very early stage of differentiation in both mouse erythroleukemia  
 RT and embryonal carcinoma cells.";

RL FEBS Lett. 358:233-239 (1995).  
 RP [3]  
 RP SEQUENCE OF 1105-2460 FROM N.A.  
 RC STRAIN=CB.17 SCID; TISSUE=THYMUS;  
 RA MEDLINE=94354845; PubMed=8074693;  
 RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;  
 RT "cDNA cloning of a novel protein tyrosine phosphatase with homology to  
 cytoskeletal protein 4.1 and its expression in T-lineage cells.";  
 RL Biochem. Biophys. Res. Commun. 203:479-484 (1994).  
 RM [4]  
 RP SEQUENCE OF 2266-2372 FROM N.A.  
 RC STRAIN=BALE/C; TISSUE=BRIN;  
 RX MEDLINE=95134232; PubMed=7832766;  
 RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;  
 RT "A novel receptor-type protein tyrosine phosphatase with a single  
 catalytic domain is specifically expressed in mouse brain.";  
 RL Biochem. J. 305:499-504 (1995).  
 CC -i- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATASE + H(2)O = PROTEIN  
 TYROSINE + PHOSPHATE.  
 CC -i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -i- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN KIDNEY AND, TO A  
 LESSER EXTENT, IN LUNG, HEART, BRAIN AND TESTIS.  
 CC -i- SIMILARITY: CONTAINS A DOMAIN FOUND IN BAND 4.1, EZRIN, MOESIN,  
 RADIKIN, AND TALIN.  
 CC -i- SIMILARITY: CONTAINS 5 DISK HOMOLOGOUS REGIONS (DHR).  
 CC -i- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-  
 TYROSINE PHOSPHATASE FAMILY.  
 DR EMBL: Z32740; CAA83650.1; -  
 DR EMBL: D83966; BAA12158.1; -  
 DR EMBL: D28529; BAA05885.1; -  
 DR EMBL: Z23059; CAA80594.1; -  
 DR PIR: S40290; S40290.  
 DR PDB: 1GMI; 08-MAR-02.  
 DR MGD: MGI:103293; Pcpn13.  
 DR GO: GO:0005856; C:cytoskeleton; IEA.  
 DR GO: GO:0005871; C:kinesin complex; IEA.  
 DR GO: GO:0016787; F:hydrolyase activity; IEA.  
 DR GO: GO:0004727; F:phosphorylated protein tyrosine phosphatase act. ...; IEA.  
 DR GO: GO:0005198; F:intracellular signaling cascade; IEA.  
 DR GO: GO:0007242; P:intracellular molecule activity; IEA.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000299; PDZ\_4.1.  
 DR InterPro: IPR001478; PDZ.  
 DR InterPro: IPR000387; Tyr\_PP.  
 DR Pfam: PF00373; Band 41; 1.  
 DR Pfam: PF00595; PDZ\_5.  
 DR PRINTS: PR00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR SMART: SM00700; PRTYPHPTASE.  
 DR SMART: SM00295; B41; 1.  
 DR SMART: SM00228; PDZ; 5.  
 DR SMART: SM00194; PTPc; 1.  
 DR PROSITE: PS00660; FERM\_1; FALSE NEG.  
 DR PROSITE: PS00661; FERM\_2; FALSE\_NEG.  
 DR PROSITE: PS50057; FERM\_3; 1.  
 DR PROSITE: PS50106; PDZ; 5.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Structural protein; Cytoskeleton; Hydrolase; Repeat; Coiled coil.  
 T DOMAIN 577 872  
 T DOMAIN 2203 2460  
 T ACT SITE 2374 2374  
 T BY SIMILARITY  
 T REPEAT 1084 1940  
 T REPEAT 1357 1441  
 T REPEAT 1490 1577  
 T REPEAT 1763 1843  
 T REPEAT 1858 1940  
 T DOMAIN 371 394  
 T COILED COIL (POTENTIAL).  
 T DOMAIN 458 493  
 T COILED COIL (POTENTIAL).  
 T POLY-LEU. 59

FT CONFLICT 79 81 STA -> FTG (IN REF. 2).  
 FT CONFLICT 156 168 HIRNSCAPSPN -> TSGTASRAFSY (IN REF.  
 2).  
 FT CONFLICT 233 233 V -> L (IN REF. 2).  
 FT CONFLICT 306 306 N -> I (IN REF. 2).  
 FT CONFLICT 322 322 K -> E (IN REF. 2).  
 FT CONFLICT 381 381 Q -> K (IN REF. 2).  
 FT CONFLICT 822 822 S -> L (IN REF. 2).  
 FT CONFLICT 1233 1233 S -> T (IN REF. 2).  
 FT CONFLICT 1449 1449 R -> Q (IN REF. 2).  
 FT CONFLICT 1474 1488 KHPMSKTALLKII -> QTPHVKDYSFVTERDNT (IN  
 REF. 2 AND 3).  
 FT CONFLICT 1621 1621 D -> H (IN REF. 2).  
 FT CONFLICT 1871 1871 P -> S (IN REF. 2 AND 3).  
 FT CONFLICT 1978 1978 N -> I (IN REF. 3).  
 FT CONFLICT 2077 2077 D -> N (IN REF. 2).  
 FT CONFLICT 2232 2232 S -> T (IN REF. 2).  
 FT CONFLICT 2445 2445 Q -> QPGLPQ (IN REF. 2 AND 3).  
 FT CONFLICT 2460 2460 MISSING (IN REF. 2 AND 3).  
 SQ SEQUENCE 2460 AA; 270965 MW; 52F29DE37DE5C807 CRC64;  
 Query Match 28.4%; Score 606; DB 11; Length 2460;  
 Best Local Similarity 31.8%; Pred. No. 3.7e-38;  
 Matches 158; Conservative 70; Mismatches 149; Indels 120; Gaps 13;  
 QY 1 MSSRR--KYRGKTGRDNDDEEGNSGNLANSPLSSQKMTPTKPIFGKMSKNYK--- 55  
 DB 1952 ISAPRFTKANGLTSM-----PSGQALPMKNSP--SKVNGEGVHEAV 1992  
 QY 56 -PSRHLSPDSKYL-----VYPPLESDDTDVTWVDYSDSLRNRMNSM-- 97  
 DB 1993 CPAGEGSSQKESAGLTETKESNRDDDIYDPQAEVIOQLDVVDEAQLNQREA 2052  
 QY 98 -----DSETAGPSKTVSPVLSSGSLSK--- 120  
 DB 2053 TRRACSPDLTNGEAPDEBGTVDYDGLPDEVPSSVSGEGKVDLASLTAASQEEKPIE 2112  
 QY 121 -----DTETS-----VSEKELQALQIRPLIFNSSARSAMRDCLNTLO- 158  
 DB 2113 EDATQESNSTTTTGDSSDKPPPTNEELALPVRVPPSGKVTGLQATITLQG 2172  
 QY 159 -----KKEHLDITREFLELEQMTLPDDFNSGHTLONRDKRYRDILPYDSTVPLGKWK 212  
 DB 2173 LLDQGIPEKLENOELKPLDQCLI-----GQTKENRKNRYKNLPYDTTRVPLGDBG 2226  
 QY 213 DVINASYIRIVNHEEYFYATQCPLETIEDFWQVLENNCNVIANITRETECGVKCY 272  
 DB 2227 GYNASRIRIPVGTQEFVYIACQGLPTTVGDVFWQVWEQNSTVIAMTQEVGEKIKQ 2286  
 QY 273 SYWPISL-KEPLEPEHFSVFLETHVTHQYFTTVFVFOIVKSKGKSCVCHLOFTKWPDHG 331  
 DB 2287 RYWPISLGTTTMANERLRLALRMQKGFVWRMALEDIQTGEVVRHISHLNFTAMPDHD 2346  
 QY 332 TPASAD---PFKYRVYRKSHITGPLLHVCAGVGTGVFCVCDVVPVSAIKNYSFDM 388  
 DB 2347 TPSQPDLLTFISYMRHRS---GPVTHCSAGIGRSGTLICIDVVLGLISQDLFFDIS 2403  
 QY 389 NIVTQMRKQRCGMIOTK 405  
 DB 2404 DLVRCMLQRHGMVQTE 2420  
 RESULT 4  
 Q28006 PRELIMINARY; PRT; 2484 AA.  
 AC Q28006  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE BA14.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

AC	Q8N4S3;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DE	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBJ_TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Renal adenocarcinoma;
RA	Strausberg R.;
RL	Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC033716.1:
DR	GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR	GO; GO:0005488; F:binding; IEA.
DR	GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR	GO; GO:0006810; P:transport; IEA.
DR	InterPro; IPR001993; Mitoch_carrier.
DR	InterPro; IPR003595; PTPC motif.
DR	InterPro; IPR000387; TYR_phosphatase.
DR	InterPro; IPR000242; Tyr_PP.
DR	Pfam; PF00102; Y_Phsphatase; 1.
DR	PRINTS; PR00700; PTYPHPTASE.
DR	SMART; SMO0194; PTEC; 1.
DR	SMART; SMO0404; PTEC_motif; 1.
DR	PROSITE; PS00215; MITOCH_CARRIER; 1.
DR	PROSITE; PS00383; TYR_PHOSPATASE_1; 1.
DR	PROSITE; PS00056; TYR_PHOSPATASE_2; 1.
DR	PROSITE; PS00055; TYR_PHOSPATASE_FTP; 1.
KW	Hypothetical protein.
FT	NON_TER
SC	SEQUENCE 292 AA; 33121 MW; 548938BDD4D1BD7 CRC64;
Query Match	21.9%; Score 468; DB 4; Length 292;
Best Local Similarity	42.3%; Pred.No.1.3e-28;
Matches	96; Conservative 35; Mismatches 78; Indels 18; Gaps 5;
QY	188 QNRDNRYRDILPDSTFVPLGKNDYINASYI-----RVNHHEEYFYIATQGPLE 240           :           :           :           :           48 QLNDKNYKDVLVDITRVLLOGNEDYINASVNNWEIPAANLVNK----YIATQGPLPH 102
DB	
QY	241 TIEDFQMWLENNCNVTAMITRIEGCVTKCYSPISKPELFEEH--FSVFLETFAVT 298           :           :           :           :           103 TCAQFWQVWDQLSLGLVMLLTTEGRTRKCQYWPK---DPDVNNHGFGFIQCSESDCT 159
DB	
QY	299 QYFTVRVPQIVKKSKGSQCXHLQTFKPFDGHGTASADFFIKYYVYRKSHI-TGPSLLV 357           :           :           :           :           160 IAYVSREMLVNICTGEHTVTELQVAMPDHGVDPDSSDFLEFNYSRLRVDSPEVLV 219
DB	
QY	358 HCSGAGVGRTGFICVDVVPSAIERNYSFDIMNVITQMKGRCMQLQT 404           :           :           :           :           220 HCSGAGIGRTGVLTMTETAMLCLTERNLPIYPELDIVVKQRDQRANNVOT 266
DB	
RESULT 6	
Q9NWU22	
ID	Q9NWU22 PRELIMINARY; PRT; 926 AA.
AC	Q9WU22;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DE	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Testis-enriched protein tyrosine phosphatase. PTPN4.
GN	Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBJ_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Testis;

CA	RN	{1}	SEQUENCE FROM N.A.
RC	RP		TISSUE=Testis;

```

RX MEDLINE=20510023; PubMed=11054567;
RA Park K.W., Lee E.J., Lee S.H., Kim B.J.,
RA Huang R., Park K.A., Baik J.H.;
RT "Molecular cloning and characterization of a protein tyrosine
RT phosphatase enriched in testis, a putative murine homologue of human
RT PTPN22."
CC Gene 257:45-55(2000).
CC -I- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF106702; AAD22773.1; -.
DR HSSP; P29350; 1GWZ.
DR MGD; MGI:1099792; Ptpn4.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00595; PDZ_1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS00567; FERM_3; 1.
DR PROSITE; PS00306; PDZ_1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
CW Hydrolase.
SQ SEQUENCE 926 AA; 105713 MW; A344DAD4PF7E2AE2 CRC64;

Query Match 21.7%; Score 463.5; DB 11; Length 926;
Best Local Similarity 27.1%; Pred. No. 1.5e-27;
Matches 130; Conservative 72; Mismatches 170; Indels 107; Gaps 12;

1Y 2 SSFPRVGRKXTER-----DNDEBEGSGN-LNLNRS-----LPSSOKMTPTKP 43
1b 450 SSFSQETPEDGQPPALPPKQSKNSWNIHFSNQDLVHTNESFDVRSSPEKSTPENG 509
1Y 44 IFGNKNSNVKPSHLFSKYLVEPEPLESDTETVNDVSDRLNRWNSKDSFAG 103
1b 510 IPHDLNLVLMKPDENGFRGPNVGGYDQGMPIVSRVA-----PGT 551
1Y 104 PSKTVSPVLGSSRLSKDTETSVSEKELTQLAQIRPLIFNSSARSAAMDCLNTLQKKE 163
1b 552 PADLCVPLNEGQVLLNGRDIAHTDQV-----LPKASCEKHSGLVLLVRPNVAV 607
1Y 164 DIREFLELE-----QMTLPDDFNNGNTL-----187
1b 608 DVVEKLSSEDFQVVPKAPLDSVHQDHSRLRESMIQLAEGLTGTVALQFDQLYRKKP 667
1Y 188 -----QNRDKNRDILPYDSTRVPLGKKNKDYINASYIR-----IVNHEEYF 230
1b 668 GMTMSACKLPQMSKNRYDIPDYATVLLKGNEDYINAYINWEIPSSLIHQ-----722
1Y 231 YIATQGPPELTEDFQWMLNENCNVAMITREICGVIKCYSWPISLKEPLEFHPFSV 290
1b 723 YIACQGPLHTCKDFQWQIMWEGQSMVMTLTQVERGRVKCHOYWE-----EPSSESSYGC 778
1Y 291 FLETHPTQ---YFTVRVFOIVKXSTGKSCVKKHLOFTKWPDHGTGTPASADFFIKYVR 347
1b 779 YQATCHSSEGNPAYIFRQKTLINQEKESRLTQIQYATPDHGVDDSDFLDFVCHVR 838
1Y 348 --KSHITPGLLVHCSAGVGRGTGVCVDVVFSAIEKNYSFDIMNIVTQMRKQRCMI 404
1b 839 DQRAKGEPIIVHCSAGVGRGTGVCVDVVFSAIEKNYSFDIMNIVTQMRKQRCMI 897

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SUET 7  
10947

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ID Q09047 PRELIMINARY; PRT; 832 AA.
AC Q09047;
DT 01-NOV-1996 (TRENBUrel. 01, Created)
DT 01-NOV-1996 (TRENBUrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBUrel. 24, Last annotation update)
DE Phosphotyrosyl phosphatase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94122757; PubMed=8293038;
RA Rowley R., Lee J.M., Corbeil H.B., Charbonneau R., Jue K.,
RA Dankort D.L., Branton P.E.;
RT "Isolation of chicken phosphotyrosyl phosphatase cDNA Sequences and
RT identification of a brain-specific species related to human PTPeta.";
RL Cell. Mol. Biol. Res. 39:209-219(1993).
DR EMBL; L27625; AAA49015.1; -.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 2.
CW Hydrolase.
SQ SEQUENCE 832 AA; 93298 MW; 4A61F365BD794F3 CRC64;

Query Match 21.5%; Score 459; DB 13; Length 832;
Best Local Similarity 27.5%; Pred. No. 2.8e-27;
Matches 133; Conservative 76; Mismatches 154; Indels 120; Gaps 14;

QY 23 GNLNRLNSLPSSSKM-----TPKPIFGNKNSE-----NVK 55
Db 34 GNLFWRNATLITQPGVTWDSHLSQTSYEDYVGLKPAIVPYSGSPVSDTSDVDLE 93
QY 56 PSHLSFSDKYLVEPEPLESDTETVNDVSDRLNRWNSMDSETAGPKTVSPVLSGS 115
Db 94 LPYSTPAFSSAELPHELSLSSSGE-----YGSASAEVLSTQTPYNEA 140
QY 116 SRLSKDTETSVSEKELTQLAQIRPLIFNSSARSA-----MRDLNTLQ-----158
Db 141 SNSHRSRIGLASLSEKKTIVPLVVSALTFCIVLILVILYWRKCFOTAFHYLEDN 200
QY 159 -----KKEELDI-----IREFLELEQMT--LPDDFN 182
Db 201 TSPRVISAPPAPVPVSDVVGAIPIKHPKPVADLHASNGFSEEPETQSCVTDLGITS 260
QY 183 SGTLNDRKVRDILPYDSTRVPL-----GKKDYINASYIRIUNHEEYFYIATQ 235
Db 261 SSHPDNKNRNYINIVAYDTRVKLAQLAEKDGKLTIDYINAYVGYNKPRA--YIAA 318
QY 236 GPLPETIEDFQWMLNENCNVAMITREICGVIKCYSWPISLKEPLEFHPFSVLETF 295
Db 319 GPLKTAEDFMRMIWEHNVVEIVMTNLEKRRKCDQYWPARGSE--EYGNFLVTQKV 376
QY 296 HVTQYETVRFQI-----VKKSTGK-----SQCKHLOFTKWPDHGTGTPASADFFIKYVR 347
Db 377 HVLAYTVVFRNLTNTKIKGSKGRSSGRVVTQHYTQWDFDMGVP-----EYTLPLVIFVR 433
QY 348 KS-----HITGPLLHCSAGVGRGTGVCVDVVFSAIEKNYSFDIMNIVTQMRKQRCMI 402
Db 434 KASHAKHAGVPIVHCSAGVGRGTGVCVDVVFSAIEKNYSFDIMNIVTQMRKQRCMI 493
QY 403 QTK 405

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD45 (Fragment).
GN PTPRC.
OS Eptatretus stoutii (Pacific hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7765;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22131575; PubMed=12136341;
RA Nagata T., Suzuki T., Ohta Y., Flajnik M.F., Kasahara M.;
RT "The leukocyte common antigen (CD45) of the Pacific hagfish,
RT Eptatretus stoutii: implications for the primordial function of
RT CD45."
RL Immunogenetics 54:286-291(2002).
DR EMBL; AB078869; BAC06504.1; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 2.
DR NON_TER 1
DR NON_TER 907
DR NON_TER 907
SQ SEQUENCE 907 AA; 103391 MW; 7833BAD232826C15 CRC64;

Query Match 21.2%; Score 451.5; DB 13; Length 907;
Best Local Similarity 36.5%; Pred. No. 1.2e-26;
Matches 104; Conservative 41; Mismatches 111; Indels 29; Gaps 7;

QY 134 LAQIEPLFNSARSAMRDLNTLQKKELDIIRFLELEQ--MTLPDDNSGNTLQ---188
DB 256 LLEVQPIL-----AEELQNVETKASDFKTFQBFESIPRWKSNFSKAAQ 303
QY 189 -NRDKNRYRDIPLDYSTRVPLGKN-----KDYINASYIRIYNHBEFYPIATQGLPETI 242
DB 304 PENGKNRYSDILPYDNNRVLSNGKPGSDYINASYIN--GYKESKKYICAQGPMBETA 361
QY 243 EDFQWQWLENNCNVAMITREIECGVYKYSWPISLKEPLEFEHFSVFLTEFHVTOYFT 302
DB 362 AEFWTMIWEQKTAIVIMVTRIEGGKNCYQYWPQKQKLEFKLSLV--TNNEVMLYPD 419
QY 303 VRVQIVKXSTGKSCQKHLOTKNPDGTPASADFFIKYRVYRK--SHITGPLLHVC 360
DB 420 YITKLSLHGGNSRIITHVQTKPFDGVPDPLLRLRRVLSFCNFDGPMWVHCS 479
QY 361 AGVGRGVTCVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 405
DB 480 AGVGRSGTPIAISLMELEDEGRIDVYGFVVSRLRQRCCLAVQVE 524

RESULT 15
Q8CIW2 PRELIMINARY; PRT; 1998 AA.
AC Q8CIW2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created;
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vascular endothelial protein tyrosine phosphatase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Swiss Webster;
RX MEDLINE=22220060; PubMed=12234928;
RA Nawroth R., Poell G., Ranft A., Kloep S., Samulowitz U., Fachinger G.,
RA Golding M., Shima D.T., Deutsch U., Vestweber D.;
RA "VE-PTP and VE-cadherin ectodomains interact to facilitate regulation
RT of phosphorylation and cell contacts.";
RL EMBO J. 21:4895-4895(2002).
DR EMBL; AY077755; AAL75813.1; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 16.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 16.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
DR SEQUENCE 1998 AA; 224474 MW; 537EA6501EF03E5D CRC64;

Query Match 21.2%; Score 451.5; DB 11; Length 1998;
Best Local Similarity 37.8%; Pred. No. 3.6e-26;
Matches 98; Conservative 47; Mismatches 101; Indels 13; Gaps 5;

QY 157 LQKKEELDIIRFLELEQNTLPDDNSGNTLQNRDKNRYRDIPLDYSTRVPLGK-----N 211
DB 1696 LQADSNNYLSKEYEDLKDVGRSQSCDIALPKNRKNRYNNILPYDASRVKLSNVDDPC 1755
QY 212 KDYNASYIRIYNHBEFYPIATQGLPETIEDFQWVLENNCNVAMITREIECGVLC 271
DB 1756 SDYINASYIPGNFRF--YIATQGLPETGDDDFKMAWQVHNIWVTCQVEKGRVKC 1813
QY 272 YSYWPISLKEPLEFEHFSVFLTEFHVTOYFTVRVQIV-KKSTGKSCQKHLOTKWPDH 330
DB 1814 DHYWPAD-QDPLYGDLILQWVSESVLPETWIREPKICSEBQDAHLRLIRHFHTWPDH 1872
QY 331 GTPASADFFIKYR---YVRKSHITGPLLHVCSSAGVGRGTGVCVDVWFSAIEKNVSFD 386
DB 1873 GVPETTSQSLIQVTRVRYINRSPGAGPTVHCSAGVGRGTGTFVALDRILQQLDSKDSVD 1932
QY 387 IMNIVTQMRKQRCGMIOTK 405
DB 1933 IYGAVHDLRLHRVHVQVE 1951

Search completed: June 21, 2004, 17:11:10
Job time : 50 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 17:10:07 ; Search time 58 Seconds  
(without alignments)  
1572.961 Million cell updates/sec

Title: US-09-095-478A-7

Perfect score: 2133

Sequence: 1 MSSPRKVRGKTGRDNDEEG.....DIMNIVTQKRCQGMQTK 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq 29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	405	2 AAW89251	AAW89251 Mouse PTP
2	2133	100.0	426	2 AAW89249	AAW89249 Mouse PTP
3	2104.5	98.7	463	2 AAW89250	AAW89250 Mouse PTP
4	1327	62.2	412	6 AAE37996	AAE37996 Human kin
5	1327	62.2	420	5 AAE14454	AAE14454 Human pro
6	1293.5	60.6	508	7 ADE08106	ADE08106 Novel pro
7	1231	57.7	398	5 AEG30845	ABG30845 Human Tyr
8	1231	57.7	398	5 ADD89795	ADD89795 Human DNF
9	1231	57.7	409	7 ADE08123	ADE08123 Novel pro
10	1227	57.5	561	4 AEG06042	ABG06042 Novel hum
11	992	46.5	261	6 AAE37994	AAE37994 Human kin
12	597.5	28.0	1267	4 AAG67637	AAG67637 Amino aci
13	597.5	28.0	1267	4 AAG67458	AAG67458 Amino aci
14	597	28.0	766	6 ABU70688	ABU70688 Human adi
15	597	28.0	2466	2 AAR71498	AAR71498 Human pro
16	597	28.0	2466	2 AAW75999	AAW75999 Intracell
17	597	28.0	2466	3 AAY90272	AAY90272 Human PTP
18	597	28.0	2485	3 AAB13343	AAB13343 Amino aci
19	566	26.5	122	2 AAW89252	AAW89252 Rat PTP10
20	474	22.2	913	2 AAW12522	AAW12522 Protein t
21	474	22.2	913	2 AAY25156	AAY25156 Human PTP
22	474	22.2	913	5 AAG79333	AAG79333 PTPH1. 8/
23	474	22.2	913	7 ADD2982	ADD2982 Human pro
24	460	21.6	197	6 AAE37997	AAE37997 Human kin
25	456	21.4	226	6 AAE37993	AAE37993 Human kin

26	456	21.4	291	4 AAG78282	AAG78282 Human PTP
27	455	21.3	1337	2 AAR85203	AAR85203 huDEP-1.
28	453	21.2	1450	7 ABR57182	ABR57182 Human PTP
29	453	21.2	1997	3 AAB19774	AAB19774 Human pro
30	453	21.2	1997	4 AAM78821	AAM78821 Human pro
31	453	21.2	1997	5 AAE20278	AAE20278 Human lun
32	453	21.2	1997	7 ABR57179	ABR57179 Human PTP
33	453	21.2	2002	4 AAM79805	AAM79805 Human pro
34	450.5	21.1	1175	7 ADEB3529	ADEB3529 Rat Prote
35	450.5	21.1	1175	7 ADEB1029	ADEB1029 Rat Prote
36	450.5	21.1	1175	7 ADEB1033	ADEB1033 Rat Prote
37	449	21.1	242	4 AAB59384	AAB59384 Mouse vas
38	449	21.1	579	3 AAB19773	AAB19773 Mouse vas
39	449	21.1	1495	5 ABB57380	ABB57380 Rat mucoc
40	449	21.1	1496	7 ADE57115	ADE57115 Rat Prote
41	449	21.1	1496	7 ADE57119	ADE57119 Rat Prote
42	449	21.1	1496	7 ADD47013	ADD47013 Rat Prote
43	449	21.1	1496	7 ADD47017	ADD47017 Rat Prote
44	445.5	20.9	1948	7 ADD18742	ADD18742 Human dis
45	445.5	20.9	1949	7 ADE57117	ADE57117 Human pro

## ALIGNMENTS

### RESULT 1

AAW89251  
ID AAW89251 standard; protein; 405 AA.

XX AAW89251;

XX 10-MAR-1999 (first entry)

XX Mouse PTP05 isoform #2.

XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

KW neurodegenerative disease; neuronal survival; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease.

XX Mus sp.

XX WO9849317-A2.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

XX 20-MAY-1997; 97US-0047222P.

XX 11-JUN-1997; 97US-0049477P.

XX 11-JUN-1997; 97US-0049756P.

XX 18-JUN-1997; 97US-0049914P.

XX 23-OCT-1997; 97US-0063595P.

XX (SUGEN-) SUGEN INC.

XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

PI Courtniege SA, App H, Hui TH;

XX WPI; 1999-009434/01.

XX N-PSDB; AAW81746.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

XX Claim 2; Page 158-160; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival,  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences;  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins

XX SQ Sequence 405 AA;  
 Query Match 100.0%; Score 2133; DB 2; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 1e-193;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRNSLPSSSQKMTPTKPIFGNKNNSNVKPSHHL 60  
 DB 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRNSLPSSSQKMTPTKPIFGNKNNSNVKPSHHL 60  
 QY 61 SFSDKYELVYPELESDDTETVWDVSDRLNRNWSMDSETAGPSKTVSPVLSSGSRLSK 120  
 DB 61 SFSDKYELVYPELESDDTETVWDVSDRLNRNWSMDSETAGPSKTVSPVLSSGSRLSK 120  
 QY 121 DTETSVSEKELTQAIQIRPLIFNSSARSAMRDLNTLQKKELDIIRFLEQMTLPDD 180  
 DB 121 DTETSVSEKELTQAIQIRPLIFNSSARSAMRDLNTLQKKELDIIRFLEQMTLPDD 180  
 QY 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRVNHHEEYFYIATGGLPE 240  
 DB 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRVNHHEEYFYIATGGLPE 240  
 QY 241 TIEDFWQVLNNCNVMIATREIECGVIKCYSYNWPISLKEPLEFHSVFLTEFHTVQY 300  
 DB 241 TIEDFWQVLNNCNVMIATREIECGVIKCYSYNWPISLKEPLEFHSVFLTEFHTVQY 300  
 QY 301 FTVRVFOIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVRVVRKSHITGPLLHCS 360  
 DB 301 FTVRVFOIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVRVVRKSHITGPLLHCS 360  
 QY 361 AGVGRGVFCVDVWFSAIEKNYSFDIMNIVTQMRKQRCMIQTK 405  
 DB 361 AGVGRGVFCVDVWFSAIEKNYSFDIMNIVTQMRKQRCMIQTK 405

RESULT 2  
 AAW89249  
 ID AAW89249 standard; protein; 426 AA.  
 XX  
 AC AAW89249;  
 XX  
 DT 10-MAR-1999 (first entry)  
 XX  
 DE Mouse PTP05.  
 XX  
 KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
 KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
 KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease.

XX MHS SP.  
 XX WO849317-A2.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 27-APR-1998; 98WO-US008439.  
 XX  
 PR 28-APR-1997; 97US-0044428P.  
 PR 20-MAY-1997; 97US-0047222P.

PR 11-JUN-1997; 97US-0049477P.  
 PR 11-JUN-1997; 97US-0049756P.  
 PR 18-JUN-1997; 97US-0049914P.  
 PR 23-OCT-1997; 97US-0063595P.  
 XX (SVGE-) SUGEN INC.  
 XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
 PI Courtneidge SA, App H, Hui TH;  
 PI N-PSDB; AAV81744.  
 DR MPI: 1999-009434/01.  
 XX New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 PT for identifying specific modulators for treatment and prevention of  
 PT cancer and neurodegenerative disease.  
 XX Claim 2; Page 155-157; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic  
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 CC present sequence represents mouse PTP05. The above proteins, other than  
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
 CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival,  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences;  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins

XX SQ Sequence 426 AA;  
 Query Match 100.0%; Score 2133; DB 2; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 1e-193;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRNSLPSSSQKMTPTKPIFGNKNNSNVKPSHHL 60  
 DB 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRNSLPSSSQKMTPTKPIFGNKNNSNVKPSHHL 60  
 QY 61 SFSDKYELVYPELESDDTETVWDVSDRLNRNWSMDSETAGPSKTVSPVLSSGSRLSK 120  
 DB 61 SFSDKYELVYPELESDDTETVWDVSDRLNRNWSMDSETAGPSKTVSPVLSSGSRLSK 120  
 QY 121 DTETSVSEKELTQAIQIRPLIFNSSARSAMRDLNTLQKKELDIIRFLEQMTLPDD 180  
 DB 121 DTETSVSEKELTQAIQIRPLIFNSSARSAMRDLNTLQKKELDIIRFLEQMTLPDD 180  
 QY 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRVNHHEEYFYIATGGLPE 240  
 DB 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRVNHHEEYFYIATGGLPE 240  
 QY 241 TIEDFWQVLNNCNVMIATREIECGVIKCYSYNWPISLKEPLEFHSVFLTEFHTVQY 300  
 DB 241 TIEDFWQVLNNCNVMIATREIECGVIKCYSYNWPISLKEPLEFHSVFLTEFHTVQY 300  
 QY 301 FTVRVFOIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVRVVRKSHITGPLLHCS 360  
 DB 301 FTVRVFOIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVRVVRKSHITGPLLHCS 360  
 QY 361 AGVGRGVFCVDVWFSAIEKNYSFDIMNIVTQMRKQRCMIQTK 405  
 DB 361 AGVGRGVFCVDVWFSAIEKNYSFDIMNIVTQMRKQRCMIQTK 405

RESULT 3  
 AAW89250

AAW89250 standard; protein; 463 AA.  
 AAW89250;  
 10-MAR-1999 (first entry)  
 Mouse PTP05 isoform #1.  
 PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.  
 Mus sp.  
 WO9849317-A2.  
 05-NOV-1998.  
 27-APR-1998; 98WO-US008439.  
 28-APR-1997; 97US-0044428P.  
 20-MAY-1997; 97US-0047222P.  
 11-JUN-1997; 97US-0049477P.  
 11-JUN-1997; 97US-0049756P.  
 18-JUN-1997; 97US-0049914P.  
 23-OCT-1997; 97US-0063595P.  
 (SUGS-) SUGEN INC.  
 Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D; Courtneidge SA, App H, Hui TH; WPI; 1999-009434/01.  
 N-PSDB; AAV81745.  
 New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.  
 Claim 2; Page 157-158; 193pp; English.  
 The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

Query Watch 98.7%; Score 2104.5; DB 2; Length 463;  
 Best Local Similarity 91.6%; Pred. No. 6.5e-191;  
 Matches 405; Conservative 0; Mismatches 0; Indels 37; Gaps 1;  
 1 MSSPRVKGKTRNDDEEGNSGLNLSNPSSSQKWTPTK----- 43  
 1 MSSPRVKGKTRNDDEEGNSGLNLSNPSSSQKWTPTKQVKNLAKYEEHLDILM 60  
 44 -----TFGNMNSENVKPSHLSFSDKYELVYPPLESDDTETW 83  
 61 VFLIKTIWVFKLWKGKLFENKNSENVKPSHLSFSDKYELVYPPLESDDTETW 120

QY 84 DVSDRLNRWNSMDSETAGPSTKTVSPVLSSGSRSLSKDTSTSVSEKELTQLAQIRPLIFN 143  
 DB 121 DVSDRLNRWNSMDSETAGPSTKTVSPVLSSGSRSLSKDTSTSVSEKELTQLAQIRPLIFN 180  
 QY 144 SSARSAMRDCNTLQKXEBELDIIREFLELEQMTLPDPFNSGNTLQNRDKNRYRDLIPYDS 203  
 DB 181 SSARSAMRDCNTLQKXEBELDIIREFLELEQMTLPDPFNSGNTLQNRDKNRYRDLIPYDS 240  
 QY 204 TRVPLGKXKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFQWVLENNCNVIAITRE 263  
 DB 241 TRVPLGKXKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFQWVLENNCNVIAITRE 300  
 QY 264 IECGVIKCYSWPISLKEPLEFEHFSVLETHVTOYFTVRVFOIVKSGTQSKQCVKHQ 323  
 DB 301 IECGVIKCYSWPISLKEPLEFEHFSVLETHVTOYFTVRVFOIVKSGTQSKQCVKHQ 360  
 QY 324 FTKWPDHGTASADFFIKYVYVRKSHITGPLLHVCSAGVGTGTFICVDVVFSAIEKNY 383  
 DB 361 FTKWPDHGTASADFFIKYVYVRKSHITGPLLHVCSAGVGTGTFICVDVVFSAIEKNY 420  
 QY 384 SFDIMNIVTQMKQRCGMIOQTK 405  
 DB 421 SFDIMNIVTQMKQRCGMIOQTK 442  
 RESULT 4  
 AAE37996  
 ID AAE37996 standard; protein; 412 AA.  
 XX  
 AC AAE37996;  
 DT 06-NOV-2003 (first entry)  
 XX Human kinase and phosphatase (KPP-41) protein.  
 DE  
 XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; neutropenic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.  
 OS Homo sapiens.  
 PN WO2003050084-A2.  
 XX 19-JUN-2003.  
 PD  
 XX 06-DEC-2002; 2002WO-US039126.  
 PF  
 XX 07-DEC-2001; 2001US-0340235P.  
 PR 19-DEC-2001; 2001US-0343007P.  
 PR 21-DEC-2001; 2001US-0343546P.  
 PR 04-FEB-2002; 2002US-0354388P.  
 PR 15-FEB-2002; 2002US-0357675P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;  
 PI Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;  
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;  
 PI Becha SD, Lee SY, Sprague WW, Zabarjadian Y;  
 XX WPI; 2003-532894/50.  
 DR N-PSDB; AAD57368.  
 XX  
 PT New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders

(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; Page 243-244; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase and phosphate (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein

Sequence 412 AA;

Query Match 62.2%; Score 1327; DB 6; Length 412;

Best Local Similarity 63.5%; Pred. No. 4.6e-117;

Matches 258; Conservative 51; Mismatches 89; Indels 8; Gaps 2;

1 MSSPRKVRGKTGDNDEBNGSNLNLNSLSSOKMTPTKPLFGKKNSENVKPSHLL 60  
 1 MSSPRFRAEPVNDYSGNSEADLNPRETLSSSQENTPSKVFENKSEKVLRLN 60  
 61 SPSDKYELVPEPLSDTETVNDVSDSLNRNMSDSETAGPSKTVSPVLSGSSRLSK 120  
 61 PPNEDYEDVFEPSSESGSDPSMTARGPPRRDRWSSEDEEAAGFSQALSPLLS 113  
 121 DTETSVSEKLTQAIRPLFNSSARSAMRDLNLTQK-EEGLDITREFLEQMTLPD 179  
 114 DTRKIVSEGLDQAIRPLFNHETQAKDLKLEKTAANDVQWEPALKEKLNLP 173  
 180 DFNSGNTLQNRKVRDILPYDSTRVPLGKVKYINASYIRIVNHEEYFYIATQGLP 239  
 174 EFNSSGQPSNRKVRDILPYDSTRVPLGKVKYINASYIRIVNHEEYFYIATQGLP 233  
 240 ETIEDFWQVLENNCHVMIATREIECGVICKYSYWPISLKEPFEHFSVLETHVQ 299  
 234 STIDDFWQVLENNCHVMIATREIEGGIKTHWPISLKEPFEHFSVLETHVQ 293  
 300 YFTVRVQIVKSTGKSCQVGHLOFTKWPDPHGTTPASADFFIKYVYRKSHITGLPLVHC 359  
 294 YFTIRFQVVEKSTGTSVSKQLQFTKWPDPHGTTPASADFFIKYVYRKSHITGLPMVHC 353  
 360 SAGVGTGTPICVDVVFSAIEKNYSFDIMNIVTQMRKORCGMOTK 405  
 354 SAGIGTGVFLCVDVVFCAIVNCSEFNIMDIVAQMRQSRGVQTK 399

RESULT 5

AAE14454

D AAE14454 standard; protein; 420 AA.

C AAE14454;

X AAE14454;

26-MAR-2002 (first entry)

X Human protein phosphatase-4.

X Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;

X neurological disorder; developmental disorder; Alzheimer's disease;

KW

KW

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OS

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cell proliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma; leukaemia; transgenic animal; gene therapy.

Homo sapiens.

Location/Qualifiers

183..411

/note="Protein-tyrosine phosphatase"

340..388

Active-site /note="Tyrosine specific protein phosphatase active site"

351..363

Region /note="Tyr\_phosphatase"

362..379

Domain /label="Transmembrane\_domain"

WO200196546-A2.

20-DEC-2001.

14-JUN-2001; 2001WO-US019442.

16-JUN-2000; 2000US-0212447P.

22-JUN-2000; 2000US-0213746P.

29-JUN-2000; 2000US-0215210P.

06-JUL-2000; 2000US-0216529P.

12-JUL-2000; 2000US-0218080P.

21-JUL-2000; 2000US-0220117P.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;

Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;

Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;

Tribouley CM, Walla NK, Yang J, Yao MG, Yue H;

WPI; 2002-090206/12.

N-PSDB; AAD24022.

Novel polypeptide, useful for diagnosing, treating or preventing

disorders of growth and development, immune system, neurological and cell

proliferation diseases, comprises cancer protein phosphatase

polypeptides.

Claim 1; Page 105-106; 116pp; English.

The present sequence is human protein phosphatase (PP)-4. PP

polynucleotide and polypeptide are useful in the diagnosis, treatment and

prevention of immune system disorders, neurological disorders,

developmental disorders and cell proliferative disorders. Examples of

immune system disorders include acquired immune deficiency syndrome

(AIDS), severe combined immunodeficiency disease (SCID), adult

respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,

atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,

emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple

sclerosis, myasthenia gravis, myocardial or pericardial inflammation,

osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,

rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic

sclerosis, trauma; neurological disorders include Alzheimer's disease,

Huntington's disease, dementia, epilepsy, Parkinson's disease, mental

retardation and other developmental disorders of central nervous system

such as Down's syndrome, cerebral palsy, periodic paralysis, mental

disorders including mood, anxiety, and schizophrenic disorders, seasonal

affective disorder such as akathisia, amnesia, cataplexy, dyskinesia;

developmental disorders include e.g. renal tubular acidosis, Duchenne and

Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell

proliferative disorders include e.g. actinic keratosis, arteriosclerosis,

atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer

including adenocarcinoma, leukaemia. The polypeptide and polynucleotide

are further useful for analysing proteome of a tissue or a cell type, for

screening an agonist/antagonist, a compound that specifically binds to it

or its modulator. The polynucleotide is useful for creating knockin





XX WO200242435-A2.  
XX 30-MAY-2002.  
XX 27-NOV-2001; 2001WO-EP013794.  
XX 27-NOV-2000; 2000US-0252912P.  
XX (FARB ) BAYER AG.  
XX Zhu Z;  
XX WPI; 2002-575236/61.  
XX N-PSDB; ABK89178.  
XX New human tyrosine phosphatase polypeptide, the regulation of which is  
XX useful for treating obesity, diabetes, cardiovascular or central nervous  
XX system disorder, chronic obstructive pulmonary disease and cancer.  
XX Claim 25; Fig 2; 145pp; English.  
XX The present invention relates to a new human tyrosine phosphatase  
XX polypeptide. The invention is useful for the preparation of a medicament  
XX for modulating the activity of human tyrosine phosphatase in a disease  
XX such as obesity, diabetes, a central nervous system (CNS) disorder,  
XX chronic obstructive pulmonary disease, cardiovascular disorder or cancer.  
XX The invention is useful for treating a human tyrosine phosphatase  
XX dysfunction related disease, preferably the above mentioned diseases. The  
XX invention is useful for treating the above mentioned disorders, where the  
XX CNS disorder is selected from Parkinson's disease, multiple sclerosis,  
XX stroke, Alzheimer's disease, and Huntington's disease, and the  
XX cardiovascular disorder is selected from congestive heart failure and  
XX myocardial infarction. The molecules of the invention are useful in  
XX diagnostic assays for detecting diseases and abnormalities or  
XX susceptibility to disease and abnormalities related to the presence of  
XX mutations in the polynucleotide coding the polypeptide of the invention.  
XX The present amino acid sequence represents the human tyrosine phosphatase  
XX protein #1 of the invention. This sequence is encoded by the human  
XX tyrosine phosphatase gene located on chromosome 10  
XX Sequence 398 AA;  
XX  
XX Query Match 57.7%; Score 1231; DB 5; Length 398;  
XX Best Local Similarity 64.9%; Pred. No. 5.9e-108;  
XX Matches 238; Conservative 46; Mismatches 75; Indels 8; Gaps 2;  
QY 40 PTKPFGKNGENKPKSHLSFSDKYLVPPELESDDTDTVDVDSRLNRWNSMDS 99  
DB 18 PQAQVFENKVBKVKLSLRNPHNDYEDVFEPESESGSDPMFTARGPFRDRASSEDE 77  
QY 100 ETAGPSKTVSPVLSGSSRLSKDTSVSSEKELTQIAQIRPLIFNSSASRANRDCIANTLQK 159  
DB 78 EAAGPSQALSPLLS-----DTRKIVSEGEQDQLAQIRPLIFNHEQTAKDKLKILEE 130  
QY 160 K-BELDIREPTELEOMLPDPPNSGNTLONDKRYDILPYDSTRYPLCKKNDYINAS 218  
DB 131 KTAAYDIMEFVALEKLNLPGEFVSGNQSNEKRYRDLIPYDSTRYPLCKKNDYINAS 190  
QY 219 YIRVNHBEYFYATQGPLPTIEDFMQVLNNCNVMIAMITREICGVTKCYSYNPIS 278  
DB 191 YIRVNHBEYFYATQGPLPTIEDFMQVLNNCNVMIAMITREMEGLIKCYHYNPIS 250  
QY 279 LKPELEFHFHSVFLETFHVTQYTVRVQIVKSGTKSCQVKGHLOFTKWDPHGTPASADF 338  
DB 251 LKPELEFHFVLENYQLQYFIIRMFQWVEKSTGSHSVKQLQFTKWDPHGTPASADS 310  
QY 339 FIKVYVYRKSHITGPLLAVHCSAGVGTGVTICVDWFSATKKNYSFDIMNIVTQMKOR 398  
DB 311 FIKYIIRAKSHLTGPMVHCSAGIGRTGVTLCVDWFCALVDCSFNIMDIVAQMEQR 370  
QY 399 CGMIQTK 405  
XX  
XX Db 371 SGMVQTK 377  
XX  
XX RESULT 8  
XX ADD89795  
XX ID ADD89795 standard; protein; 398 AA.  
XX AC ADD89795;  
XX DT 29-JAN-2004 (first entry)  
XX DE Human DKFZP566K0524 protein SEQ ID NO:10.  
XX KW cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;  
XX immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
XX antiarthritic; antiapoptotic; antiarteriosclerotic; antiinflammatory;  
XX vulnary; gynaecological; angiogenic; hyperproliferative disease;  
XX autoimmune disease; diabetes mellitus; multiple sclerosis;  
XX rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;  
XX endometriosis; angiogenesis.  
XX OS Homo sapiens.  
XX WO2003083102-A2.  
XX 09-OCT-2003.  
XX 19-MAR-2003; 2003WO-CA000393.  
XX 28-MAR-2002; 2002US-0368859P.  
XX (KINE-) KINETEK PHARM INC.  
XX Delaney AD;  
XX WPI; 2003-902934/82.  
XX N-PSDB; ADD89794.  
XX New nucleic acids encoding cancer associated phosphatases, useful as  
XX targets for screening pharmaceutical agents that inhibit the growth of  
XX tumor cells, or for diagnosing and treating cancer, inflammation or  
XX autoimmune disease.  
XX Claim 1; SEQ ID NO 10; 63pp; English.  
XX The present invention describes an isolated cancer associated phosphatase  
XX nucleic acid. Also described: (1) a method of screening for biologically  
XX active agents that modulate a cancer associated phosphatase function; (2)  
XX a method for the diagnosis of cancer; (3) a method for inhibiting the  
XX growth of a cancer cell; (4) methods of screening for targets of a cancer  
XX associated phosphatase, where the targets are associated with signal  
XX transduction in cancer cells; (5) a compound (C) for the treatment of a  
XX tumour; (6) a composition for the treatment of a tumour comprising a  
XX pharmaceutical carrier and (C); (7) methods for treating a tumour; and  
XX (8) a method for visualising a tumour in a patient. A cancer associated  
XX phosphatase of the present invention has cytostatic, immunosuppressive,  
XX antidiabetic, neuroprotective, antirheumatic, antiarthritic,  
XX antiapoptotic, antiarteriosclerotic, antiinflammatory, vulnary,  
XX gynaecological and angiogenic activities. The cancer associated  
XX phosphatases and nucleic acids encoding the proteins are useful for  
XX visualising tumours in patients or diagnosing and treating cancer, e.g.  
XX pancreas, lung, ovarian, liver or colon cancer. The polypeptides and  
XX nucleic acids may also be used for treating hyperproliferative diseases,  
XX such as autoimmune disease, diabetes mellitus, multiple sclerosis,  
XX rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring,  
XX endometriosis or angiogenesis, determining the effectiveness of drugs,  
XX determining patient prognosis, or as targets for screening pharmaceutical  
XX agents that inhibit the growth or metastasis of tumour cells. The present  
XX sequence represents the human cancer associated phosphatase  
XX DKFZP566K0524, which is used in the exemplification of the present  
XX invention.  
XX Sequence 398 AA;

Downloaded from <http://ajph.org/> on November 10, 2014

Downloaded from <http://ajph.org/> on November 10, 2014

\_\_\_\_\_







AAR71498  
ID AAR71498 standard; protein; 2466 AA.

AC AAR71498;  
AC AAR71498;

DT 25-MAR-2003 (revised)  
DT 05-OCT-1995 (first entry)

XX Human protein tyrosine phosphatase PTPPL1.  
DB 05-OCT-1995 (first entry)

XX Protein tyrosine phosphatase; PTPPL1.  
KW Protein tyrosine phosphatase; PTPPL1.

XX Homo sapiens.  
OS Homo sapiens.

XX Key  
FH Region Location/Qualifiers  
FT 470..505  
FT /label= leucine zipper motif  
FT 570..885  
FT Region  
FT /notes= "homology to the band 4.1 superfamily"

XX WO9506735-A2.  
PN WO9506735-A2.

XX 09-MAR-1995.  
PD 09-MAR-1995.

XX 01-SEP-1994; 94MO-US009943.  
XX 01-SEP-1994; 94MO-US009943.

XX 01-SEP-1993; 93US-00115573.  
XX 01-SEP-1993; 93US-00115573.

XX (LUDW-) LUDWIG INST CANCER RES.  
XX (LUDW-) LUDWIG INST CANCER RES.

XX Genez LJ, Saras J, Claesson-Welsh L, Heidin C;  
XX Genez LJ, Saras J, Claesson-Welsh L, Heidin C;

XX NPI; 1995-115450/15.  
XX NPI; 1995-115450/15.

XX N-PSDB; AAQ85924.  
XX N-PSDB; AAQ85924.

XX New protein tyrosine phosphatase(s), PTPPL1 and GLM-2 - used to develop  
XX New protein tyrosine phosphatase(s), PTPPL1 and GLM-2 - used to develop

XX prods. for use in detection, diagnosis, screening assays or therapy.  
XX prods. for use in detection, diagnosis, screening assays or therapy.

XX Claim 9; Page 56-68; 92pp; English.  
XX Claim 9; Page 56-68; 92pp; English.

XX A cDNA library was prep'd. from human glioma cell line U-343 MGA 31L or  
XX A cDNA library was prep'd. from human glioma cell line U-343 MGA 31L or

XX Ag1518 human foreskin fibroblasts. Degenerate primers based on conserved  
XX Ag1518 human foreskin fibroblasts. Degenerate primers based on conserved

XX regions of PTPs were prep'd. Sense oligos were AAQ85926 and AAQ85927, and  
XX regions of PTPs were prep'd. Sense oligos were AAQ85926 and AAQ85927, and

XX the antisense oligo was AAQ85928. Three clones defined novel PTP  
XX the antisense oligo was AAQ85928. Three clones defined novel PTP

XX sequences. Two of these were named PTPPL1 and GLM-2. The U-343 MGA 31L  
XX sequences. Two of these were named PTPPL1 and GLM-2. The U-343 MGA 31L

XX cDNA library was screened with labeled probes corresp. to PTPPL1. The  
XX cDNA library was screened with labeled probes corresp. to PTPPL1. The

XX Ag1518 human fibroblast cDNA library was also screened. The complete ORF  
XX Ag1518 human fibroblast cDNA library was also screened. The complete ORF

XX of PTPPL1 was derived from six overlapping cDNA clones and is given in  
XX of PTPPL1 was derived from six overlapping cDNA clones and is given in

XX AAQ85924. (Updated on 25-MAR-2003 to correct PN field.)  
XX AAQ85924. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 2466 AA;  
XX Sequence 2466 AA;

Query Match 28.0%; Score 597; DB 2; Length 2466;  
Query Match 28.0%; Score 597; DB 2; Length 2466;

Best Local Similarity 33.8%; Pred. No. 2e-46;  
Best Local Similarity 33.8%; Pred. No. 2e-46;

Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;  
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;

Y 6 KVRGKTGRDNDEEGNSGNLRLNSLP---SSQKMTPTKPIFGNKNNSNVKPSHLSF 62  
Y 6 KVRGKTGRDNDEEGNSGNLRLNSLP---SSQKMTPTKPIFGNKNNSNVKPSHLSF 62

b 2070 KXGKLSEERTDTCDG-----SPLPYPTATKMGCEYCEKVKSESL----- 2116  
b 2070 KXGKLSEERTDTCDG-----SPLPYPTATKMGCEYCEKVKSESL----- 2116

Y 63 SDKVELVPEPLESDPTDTPVDVDSRLRNWNSDSETAGPSKTVSPVLSGSSRLSKOT 122  
Y 63 SDKVELVPEPLESDPTDTPVDVDSRLRNWNSDSETAGPSKTVSPVLSGSSRLSKOT 122

b 2117 -----IQKPEKKTDDDEITWG-NDELPFIRTNHSDS-----KD- 2150  
b 2117 -----IQKPEKKTDDDEITWG-NDELPFIRTNHSDS-----KD- 2150

Y 123 ETSVSEKELTQLAQLRPLFNSSARSAMRDCNLTQ-----KXELDIIRFLELEQM 175  
Y 123 ETSVSEKELTQLAQLRPLFNSSARSAMRDCNLTQ-----KXELDIIRFLELEQM 175

b 2151 HSFLTNDLAVLPVVKVLPVSGRYTGANLKVIRVLRLGLDQGPSKELENLQELKPLDQC 2210  
b 2151 HSFLTNDLAVLPVVKVLPVSGRYTGANLKVIRVLRLGLDQGPSKELENLQELKPLDQC 2210

Y 176 TLPPDDNSGNTLQNRDKRYDILPYDSTRVPLGKNKYDINASYIRVWNEHEEYFYIATQ 235  
Y 176 TLPPDDNSGNTLQNRDKRYDILPYDSTRVPLGKNKYDINASYIRVWNEHEEYFYIATQ 235

c 2211 LI-----GCTENRKNRYKNILPYDSTRVPLGDEGYINASFIPVKGKREYFIATQ 2264  
c 2211 LI-----GCTENRKNRYKNILPYDSTRVPLGDEGYINASFIPVKGKREYFIATQ 2264

Y 236 GPLPETIEDFWQVLENNCNVMIATREIECGVICKYSYMPISL-KEPFEFEHFSVFLET 294  
Y 236 GPLPETIEDFWQVLENNCNVMIATREIECGVICKYSYMPISL-KEPFEFEHFSVFLET 294

Db 2365 GELPTTWGDFWQMIWEQKSTVIAMTQVEGEKIKQRYWPHILGKTTWVSNRLRLALVR 2324  
QY 2395 FHVTOYETVAVFQIVKKSTGKSCQVKHLOFTKWPDHGTASADFFIKVRYVRKSHITGP 354  
Db 2325 MQQLKGFVVRAMTLEDIOITREVRHISHLNFTAMPDHDTPSQPDDLITFISYWRHHRSGP 2384  
QY 355 LLVHCSAGVGTGVFICVDVWVPSAIEKNYSFDIMNIVTOMRKORCGMIQTK 405  
Db 2385 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRCVRLQRHGMVQTE 2435

Search completed: June 21, 2004, 17:12:56  
Job time : 62 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: June 21, 2004, 17:11:16 ; Search time 48 seconds  
(without alignments)  
2382.021 Million cell updates/sec

Title: US-09-095-478A-7

Perfect score: 2133

Sequence: 1 MSSPRVGRGTGNDDEBGG.....DIMNIVTMRKQRCGMIIQTK 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubaa/ECT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubaa/ECT05\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	412	10	US-09-095-478-3
2	2133	100.0	426	10	US-09-095-478-1
3	2104.5	98.1	463	10	US-09-095-478-2
4	1900	89.1	379	10	US-09-095-478-8
5	1765	82.7	354	10	US-09-095-478-6
6	1327	62.2	422	16	US-10-311-764-4
7	668	31.3	122	10	US-09-095-478-4
8	597.5	28.0	1267	12	US-10-060-065-35
9	597.5	28.0	1267	14	US-10-059-585-56
10	597	28.0	2465	14	US-10-177-980-12
11	597	28.0	2485	9	US-09-802-669-46
12	597	28.0	2485	12	US-10-619-220-46
13	597	28.0	2485	16	US-10-408-765A-1349
14	590.5	27.7	381	10	US-09-095-478-7
15	584	27.4	358	10	US-09-095-478-9

16	566	26.5	122	10	US-09-095-478-5
17	541.5	25.4	263	12	US-10-087-684-93
18	541.5	25.4	263	12	US-10-218-779-93
19	499	23.4	235	12	US-10-087-684-94
20	499	23.4	235	12	US-10-218-779-94
21	499	23.4	235	12	US-10-072-012-819
22	474	22.2	703	15	US-10-366-547-40
23	474	22.2	913	9	US-09-848-294-2
24	474	22.2	913	14	US-10-293-231-2
25	474	22.2	913	15	US-10-366-547-38
26	462	21.7	244	9	US-09-848-294-7
27	462	21.7	244	14	US-10-293-231-7
28	456	21.4	291	9	US-09-788-626-22
29	455	21.3	1337	14	US-10-390-501-2
30	455	21.3	1337	15	US-10-366-547-42
31	455	21.3	1337	15	US-10-366-547-44
32	453	21.2	1997	10	US-09-909-567B-54
33	453	21.2	1997	16	US-10-634-027-2
34	453	21.2	1997	16	US-10-408-765A-2135
35	449.5	21.1	312	16	US-10-634-027-6
36	449.5	21.1	319	16	US-10-634-027-7
37	449.5	21.1	336	16	US-10-634-027-4
38	449	21.1	1495	15	US-10-258-566-12
39	445.5	20.9	1948	9	US-09-808-602-55
40	445.5	20.9	1948	10	US-09-800-198-45
41	445	20.9	1105	12	US-10-296-115-1082
42	444	20.8	1216	15	US-10-366-547-49
43	443	20.8	1238	15	US-10-366-547-47
44	442.5	20.7	264	14	US-10-245-539-6
45	442	20.7	1463	14	US-10-176-847-22

#### ALIGNMENTS

#### RESULT 1

US-09-095-478-3  
; Sequence 3, Application US/09095478  
; Publication No. US20030095970A1  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory  
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND  
; TITLE OF INVENTION: RELATED PRODUCTS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 224/115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600

Sequence 5, Appli  
Sequence 93, Appli  
Sequence 93, Appli  
Sequence 94, Appli  
Sequence 94, Appli  
Sequence 94, Appli  
Sequence 819, Appli  
Sequence 40, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 38, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 22, Appli  
Sequence 2, Appli  
Sequence 42, Appli  
Sequence 44, Appli  
Sequence 54, Appli  
Sequence 2, Appli  
Sequence 2135, Ap  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 4, Appli  
Sequence 12, Appli  
Sequence 55, Appli  
Sequence 45, Appli  
Sequence 1082, Ap  
Sequence 49, Appli  
Sequence 47, Appli  
Sequence 6, Appli  
Sequence 22, Appli

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-3

Query Match      100.0%; Score 2133; DB 10; Length 412;
Best Local Similarity 100.0%; Pred. No. 5,7e-185;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDEEGNSGNLNRNSLPSSQKMTPTKPIFGNKWNSNVKPSHHL 60
DB 1 MSSPRKVRGKTGRDNDEEGNSGNLNRNSLPSSQKMTPTKPIFGNKWNSNVKPSHHL 60
QY 61 SFSKVELVYPEPLESDTDTETVMDVSDRLNRNWNMSDSETAGPSKTVSPVLGSSRLSK 120
DB 61 SFSKVELVYPEPLESDTDTETVMDVSDRLNRNWNMSDSETAGPSKTVSPVLGSSRLSK 120
QY 121 DTETSVSEKELTOLAQIRPLIFNSSARSAMRDCNLTLOKKELDIIRFLELEQMTLPDD 180
DB 121 DTETSVSEKELTOLAQIRPLIFNSSARSAMRDCNLTLOKKELDIIRFLELEQMTLPDD 180
QY 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGNKDYINASYIRVNWHEEYFYIATQGPLPE 240
DB 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGNKDYINASYIRVNWHEEYFYIATQGPLPE 240
QY 241 TIEDFWQVLENNCNVIAITREIEGCVIKCYSYNPISLKEPFEHPSVLETHVTOY 300
DB 241 TIEDFWQVLENNCNVIAITREIEGCVIKCYSYNPISLKEPFEHPSVLETHVTOY 300
QY 301 FTVRVFIQVKSTGKSCQVKHLOFTKWDHGTGPASADFFIKYVYVRKSHITGPLLHCS 360
DB 301 FTVRVFIQVKSTGKSCQVKHLOFTKWDHGTGPASADFFIKYVYVRKSHITGPLLHCS 360
QY 361 AGVGRGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOYK 405
DB 361 AGVGRGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOYK 405

```

## RESULT 2

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US-09-095-478-1
; Sequence 1, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-1

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Query Match      100.0%; Score 2133; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 6e-185;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDEEGNSGNLNRNSLPSSQKMTPTKPIFGNKWNSNVKPSHHL 60
DB 1 MSSPRKVRGKTGRDNDEEGNSGNLNRNSLPSSQKMTPTKPIFGNKWNSNVKPSHHL 60
QY 61 SFSKVELVYPEPLESDTDTETVMDVSDRLNRNWNMSDSETAGPSKTVSPVLGSSRLSK 120
DB 61 SFSKVELVYPEPLESDTDTETVMDVSDRLNRNWNMSDSETAGPSKTVSPVLGSSRLSK 120
QY 121 DTETSVSEKELTOLAQIRPLIFNSSARSAMRDCNLTLOKKELDIIRFLELEQMTLPDD 180
DB 121 DTETSVSEKELTOLAQIRPLIFNSSARSAMRDCNLTLOKKELDIIRFLELEQMTLPDD 180
QY 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGNKDYINASYIRVNWHEEYFYIATQGPLPE 240
DB 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGNKDYINASYIRVNWHEEYFYIATQGPLPE 240
QY 241 TIEDFWQVLENNCNVIAITREIEGCVIKCYSYNPISLKEPFEHPSVLETHVTOY 300
DB 241 TIEDFWQVLENNCNVIAITREIEGCVIKCYSYNPISLKEPFEHPSVLETHVTOY 300
QY 301 FTVRVFIQVKSTGKSCQVKHLOFTKWDHGTGPASADFFIKYVYVRKSHITGPLLHCS 360
DB 301 FTVRVFIQVKSTGKSCQVKHLOFTKWDHGTGPASADFFIKYVYVRKSHITGPLLHCS 360
QY 361 AGVGRGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOYK 405
DB 361 AGVGRGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOYK 405

```

## RESULT 3

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US-09-095-478-2
; Sequence 2, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 224/115  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 463 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; US-09-095-478-2

Query Match 98.7%; Score 2104.5; DB 10; Length 463;  
 Best Local Similarity 91.6%; Pred. No. 2.6e-182;  
 Matches 405; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MSSPRKVGKTRNDDEEGSGNLRLNSLPSSSQKWTPTK-----43  
 DB 1 MSSPRKVGKTRNDDEEGSGNLRLNSLPSSSQKWTPTKVNKNLKYEHLDILM 60  
 QY 44 -----IFGKNMSENKPSHLSFSDKYELVYPEPESDDETVW 83  
 DB 61 VLLIKTIWNVFKLWKGLIFGKNMSENKPSHLSFSDKYELVYPEPESDDETVW 120  
 QY 84 DVSDSLNRNWSMDSETAGSKTVSVLSGSRSLKDTSTVSSEKELTQIAQIRPLFN 143  
 DB 121 DVSDSLNRNWSMDSETAGSKTVSVLSGSRSLKDTSTVSSEKELTQIAQIRPLFN 180  
 QY 144 SSASAMRDCLNTLOKKEELDIREFLEQLMTLPDDFNSGNTLQNRDKNRYRDLPYDS 203  
 DB 181 SSASAMRDCLNTLOKKEELDIREFLEQLMTLPDDFNSGNTLQNRDKNRYRDLPYDS 240  
 QY 204 TRVPLGKNKDYINASYIRIVNHEEYFIATQGPLPETHDFWQVLENNCNVIAWITRE 263  
 DB 241 TRVPLGKNKDYINASYIRIVNHEEYFIATQGPLPETHDFWQVLENNCNVIAWITRE 300  
 QY 264 IECGVKCYSWPISLKEPELEFHFVFTVVRVQIVKSGTSGKQCVKHLQ 323  
 DB 301 IECGVKCYSWPISLKEPELEFHFVFTVVRVQIVKSGTSGKQCVKHLQ 360  
 QY 324 FTKPDHGTASADFFIKYRYVRKSHITGPLLHVCAGVGTGVFCVDVWFSIAEKY 383  
 DB 361 FTKPDHGTASADFFIKYRYVRKSHITGPLLHVCAGVGTGVFCVDVWFSIAEKY 420  
 QY 384 SFDIMNIVTQMRKQRCGMIOQTK 405  
 DB 421 SFDIMNIVTQMRKQRCGMIOQTK 442

RESULT 4  
 JS-09-095-478-8  
 ; Sequence 8, Application US/09095478  
 ; Publication No. US20030095970A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PLOWMAN, Gregory  
 ; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND  
 ; TITLE OF INVENTION: RELATED PRODUCTS AND  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/095,478  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 224/115  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 379 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; US-09-095-478-8

Query Match 89.1%; Score 1900; DB 10; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-164;  
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GNMNSENKPSHLSFSDKYELVYPEPESDDETVWVSDSLNRNWSMDSETAGPS 105  
 DB 1 GNMNSENKPSHLSFSDKYELVYPEPESDDETVWVSDSLNRNWSMDSETAGPS 60  
 QY 106 KTVSPVLSGSRSLKDTSTVSSEKELTQIAQIRPLFNSSASAMRDCLNTLOKKEELDI 165  
 DB 61 KTVSPVLSGSRSLKDTSTVSSEKELTQIAQIRPLFNSSASAMRDCLNTLOKKEELDI 120  
 QY 166 IREFLEQLMTLPDDFNSGNTLQNRDKNRYRDLFYDSTRVPLGKNKDYINASYIRIVN 225  
 DB 121 IREFLEQLMTLPDDFNSGNTLQNRDKNRYRDLFYDSTRVPLGKNKDYINASYIRIVN 180  
 QY 226 EEEFYFIATQGPLPETHDFWQVLENNCNVIAWITREIBCGVIKCYSWPISLKEPELEF 285  
 DB 181 EEEFYFIATQGPLPETHDFWQVLENNCNVIAWITREIBCGVIKCYSWPISLKEPELEF 240  
 QY 286 EHFVSFLETFHVTOYFTVVRVQIVKSGTSGKQCVKHLQFTKPDHGTASADFFIKYRY 345  
 DB 241 EHFVSFLETFHVTOYFTVVRVQIVKSGTSGKQCVKHLQFTKPDHGTASADFFIKYRY 300  
 QY 346 VRKSHITGPLLHVCAGVGTGVFCVDVWFSIAEKYNSFDIMNIVTQMRKQRCGMIOQTK 405  
 DB 301 VRKSHITGPLLHVCAGVGTGVFCVDVWFSIAEKYNSFDIMNIVTQMRKQRCGMIOQTK 360

RESULT 5  
 US-09-095-478-6

Sequence 6, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUTPOS AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Fast-Seq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-6

Query Match 82.7%; Score 1765; DB 10; Length 354;  
Best Local Similarity 100.0%; Pred. No. 1.2e-151;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 71 PEPLSDTDTVDVSDRSRLRNWNSMDSETAGPSKTVSPVLGGSSRLSKDTTSVSEKE 130  
DB 1 PEPLSDTDTVDVSDRSRLRNWNSMDSETAGPSKTVSPVLGGSSRLSKDTTSVSEKE 60  
QY 131 LTLOAQIRPLFNSASARMDCLNTLQKBEELDIREFLEQMTLPDDNSGNTLQNR 190  
DB 61 LTLOAQIRPLFNSASARMDCLNTLQKBEELDIREFLEQMTLPDDNSGNTLQNR 120  
QY 191 DKNRVRDILPYDSRTRVPLGKXKDYINASYIRIVNHEEYFYIATQGLPETIEDFQMWL 250  
DB 121 DKNRVRDILPYDSRTRVPLGKXKDYINASYIRIVNHEEYFYIATQGLPETIEDFQMWL 180  
QY 251 ENNCNVAMITREIECGVVKCYSWPISLKEPESVFELETHVQYFVRVQIVK 310  
DB 181 ENNCNVAMITREIECGVVKCYSWPISLKEPESVFELETHVQYFVRVQIVK 240  
QY 311 KSTGSKQCVKHLQTPKPDHGTASADFFIKYRVYRKSHITGPLLHVCSAGVGTGVI 370  
DB 241 KSTGSKQCVKHLQTPKPDHGTASADFFIKYRVYRKSHITGPLLHVCSAGVGTGVI 300  
QY 371 CVDVFSNIEKNYSFDIMNIVTQMEKQRCGMIOTK 405  
|||||

Db 301 CVDVFSNIEKNYSFDIMNIVTQMEKQRCGMIOTK 335  
RESULT 6  
US-10-311-764-4  
Sequence 4, Application US/10311764  
Publication No. US20040023245A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
APPLICANT: BAUGHN, Mariah R.; DING, Li  
APPLICANT: ELLIOTT, Vicki S.; GANDHI, Aneena R.  
APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.  
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
APPLICANT: LU, Yan; NGUYEN, Daniel B.  
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.  
APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.  
APPLICANT: CHAMLA, Narinder K.; YANG, Junning  
APPLICANT: YAO, Monique G.; YUE, Henry  
TITLE OF INVENTION: PROTEIN PHOSPHATASES  
FILE REFERENCE: PI-0126 USN  
CURRENT APPLICATION NUMBER: US/10/311,764  
CURRENT FILING DATE: 2002-12-16  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: PCT/US01/19442  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/212,447  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US 60/213,746  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/215,210  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/216,529  
PRIOR FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: US 60/218,080  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/220,117  
PRIOR FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PERL Program  
SEQ ID NO 4  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1  
US-10-311-764-4

Query Match 62.2%; Score 1327; DB 16; Length 420;  
Best Local Similarity 63.5%; Pred. No. 9.7e-112;  
Matches 258; Conservative 51; Mismatches 89; Indels 8; Gaps 2;  
QY 1 MSSPRKVRGKTGRDNDREEGNSGNIILNLSIPSSQKMTPTKPIFGNOMSNVVKPSHLL 60  
DB 1 MSSPRDFRAEPVNDYEGNDSEADLNTRETLPSQQENTPRSKVFENKYNSEKVKLSLN 60  
QY 61 SPDSKYELVPEPLESDTDTVDVSDRSRLRNWNSMDSETAGPSKTVSPVLGGSSRLSK 120  
DB 61 PPHNDYEDVFPPEPSGSDPSMTARGPFRDRWSSDEBEAGPSQALSPLLS----- 113  
QY 121 DTEVTSVKELTQLAQIRPLIFNSSASARMDCLNTLQK-BELDIIRBFLEQMTLPD 179  
DB 114 DTRKIVSCELDDQLAQIRPLIFNFEHQTAIDCKLSEKTAAYDIDQBPMALEKLNPG 173  
QY 180 OFNSGNTVQNKRRYRDLPYDSTRVPLGKXKDYINASYIRIVNHEEYFYIATQGLP 239  
DB 174 EFNSGNQPSNREKRYRDLPYDSTRVPLGKXKDYINASYIRIVNHEEYFYIATQGLP 233  
QY 240 ETIEDFQMWLVNCCNVAMITREIECGVVKCYSWPISLKEPESVFELETHVQ 299  
DB 234 STIDDFQMWLVNCCNVAMITREIECGVVKCYSWPISLKEPESVFELETHVQ 293  
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QY	300	YFTVRVFOIVKSTCKSCOVCHLOFTKWPDHGHTPASADPFKIVRYRKSHITGELLVHC	359
DB	294	YFIIMFQVWZKSTGTSVFSQLOFTKWPDHGHTPASADPFKIVRYRKSHLTGPMVWHC	353
QY	360	SAGVGRGTGVFCVDVWFSAIBENYSFDIMNIVTQMRQRCMIQTQ	405
DB	354	SAGIGRTGVFLCVDFVFCVCAIVKNSFIMDVAOMREORSQWOTK	399

## RESULT 7

US-09-095-478-4  
Sequence 4, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPT05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-4

## RESULT a

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US-10-060-065-35
; Sequence 35, Application US/10060065
; Publication No. US20030017480A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-029002
; CURRENT APPLICATION NUMBER: US/10/060,065
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-065-35

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## RESULTS

db 1187 ITHCSAGIGRSGTLCIDPWLGLISODLPDIPDLVRCMRLORHGMVOTE 1236

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RESULT 10
US-10-177-980-12
; Sequence 12, Application US/10177980
; Publication No. US20030166232A1
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gonez, Leonel Jorge
; APPLICANT: Haldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177.980
; CURRENT FILING DATE: 2002-06-21

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: PRIOR APPLICATION NUMBER: US/09/080,855
:
: PRIOR FILING DATE: 1998-05-18
:
: PRIOR APPLICATION NUMBER: 08/805,583
:
: PRIOR FILING DATE: 1997-02-25
:
: NUMBER OF SEQ ID NOS: 39
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 12
:
: LENGTH: 2466
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-10-177-980.12

```

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Qy 123 ETSVSEKELQOLAQIAPLIFNSAGSAMKDCINTLQ-----KKEELDIDREPLEEQM 175
      : : | | : : : : : : : : : : : : : : : : : : : : : : : : : :
2151 HSFLTDELAVLPVKVLPSGKYTGANLKSIVRVLRGLDQGISKELENLQELKPLDQC 2210
Db

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Qy	176	TLPDPNSGNTLQNDRKRYRDIILPYDSTRVPLGNKNKYINASYIRIVWHREEFYIATQ	235
Db	2211	LI-----GGTKENRKRYRNILFYDATRVPLDGEGGYINASFIKLPGKEEFVIATCQ	2264

[illegible]

Oy            295 FHVTOYFTVRFOIVKSKTSQCVKHLOFTKYWPDBGT PASADFFIKYRVRYRKSHITGP 354  
:  
:  
:  
  
Db            2325 MQLKGFWZAMTLEDIOTREVRHISHLNFTAMPDHDTPSQDDLLTFISYNRHIHRSGP 2384

```
Oy      355 LLVCSAGVGRGTVPICVDVVPSALEKNSFDIMNIVTQMEKQRCCGNIQTk 405
        ::|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      2385 IITHCSAGISRGTTICIDVVLGLISQDLDFDISLVRCMLQRHGVQTE 2435
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RESULT 11  
US-09-803-669-46

RESULT 11  
US-09-802-689-46

; Sequence 46, Application US/09802669  
; Patent No. US2002004490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/09/802,669  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US/09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 2485  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-802-669-46

Query Match 28.0%; Score 597; DB 9; Length 2485;  
Best Local Similarity 33.8%; Pred. No. 2.7e-44;  
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;

QY 6 KVRGKTGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGKNKNSENVKPSHLSF 62  
DB 2089 KXGKLSERTEDTDCG-----SPLPYFTATKNGCEYCEKVKSES- 2135

QY 63 SKYELVPEPLESDTDTVDVSDRSLSRNWNSMDSETAGSKTVSPVLSGSSRLSKDT 122  
DB 2136 -----IQKPEKKTDDDEITWG-NDELPIERTNHDSD-----KD- 2169

QY 123 ETSVSEKELTQLAQRPLIFNSSARSAMEDCLNTLQ-----KKELDIIRFPLELEQM 175  
DB 2170 HSLFTNDELAVLPVVKVLPDSGYTKANLKSIVIRVLGGLDQIGPSKLENLQELKPLDQC 2229

QY 176 TLPDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235  
DB 2230 LI-----GQTKENRRKRYKNILPYDATRVPLDGGYINASFIPKIPVKEEFYIACQ 2283

QY 236 GLPETIEDFWQVLNNCNVIAMITREICGVKICYSWPISL-KPPLFEHFSVPLET 294  
DB 2284 GLPLTVGDFWQMIWEQKSTVIAMWQVEGEKIKCQRYWENILGKTTWVSNRLRLALVR 2343

QY 295 FHVQYFTVRVFOIVKSTGKSCQVHLQFTKWDHGTGPASADFFIKYVVRVKSHTGP 354  
DB 2344 MQQLKGFVVRATLIEDIQTRVREHISHLNFTAWPDHDTGPSQDDLLTFISYMRHRS GP 2403

QY 355 LLVHCSAGVGTGFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 405  
DB 2404 IITHCSAGIGRSGTLICIDVVLGISQDLDFDIDLVRCKRLQRHGMVQTE 2454

RESULT 12  
US-10-619-220-46  
; Sequence 46, Application US/10619220  
; Publication No. US20040033979A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/10/619,220  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 09/802,669  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: US/09/665,615  
; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 2485  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-619-220-46

Query Match 28.0%; Score 597; DB 12; Length 2485;  
Best Local Similarity 33.8%; Pred. No. 2.7e-44;  
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;

QY 6 KVRGKTGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGKNKNSENVKPSHLSF 62  
DB 2089 KXGKLSERTEDTDCG-----SPLPYFTATKNGCEYCEKVKSES- 2135

QY 63 SKYELVPEPLESDTDTVDVSDRSLSRNWNSMDSETAGSKTVSPVLSGSSRLSKDT 122  
DB 2136 -----IQKPEKKTDDDEITWG-NDELPIERTNHDSD-----KD- 2169

QY 123 ETSVSEKELTQLAQRPLIFNSSARSAMEDCLNTLQ-----KKELDIIRFPLELEQM 175  
DB 2170 HSLFTNDELAVLPVVKVLPDSGYTKANLKSIVIRVLGGLDQIGPSKLENLQELKPLDQC 2229

QY 176 TLPDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQ 235  
DB 2230 LI-----GQTKENRRKRYKNILPYDATRVPLDGGYINASFIPKIPVKEEFYIACQ 2283

QY 236 GLPETIEDFWQVLNNCNVIAMITREICGVKICYSWPISL-KPPLFEHFSVPLET 294  
DB 2284 GLPLTVGDFWQMIWEQKSTVIAMWQVEGEKIKCQRYWENILGKTTWVSNRLRLALVR 2343

QY 295 FHVQYFTVRVFOIVKSTGKSCQVHLQFTKWDHGTGPASADFFIKYVVRVKSHTGP 354  
DB 2344 MQQLKGFVVRATLIEDIQTRVREHISHLNFTAWPDHDTGPSQDDLLTFISYMRHRS GP 2403

QY 355 LLVHCSAGVGTGFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 405  
DB 2404 IITHCSAGIGRSGTLICIDVVLGISQDLDFDIDLVRCKRLQRHGMVQTE 2454

RESULT 13  
US-10-408-765A-1349  
; Sequence 1349, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fany, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Wainock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1349  
; LENGTH: 2485  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1349

Query Match 28.0%; Score 597; DB 16; Length 2485;  
Best Local Similarity 33.8%; Pred. No. 2.7e-44;  
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;

QY 6 KVRGKTGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGKNKNSENVKPSHLSF 62





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 17:11:46 ; Search time 29 seconds  
(without alignments)

720.983 Million cell updates/sec

Title: US-09-095-478A-7

Perfect score: 2133

Sequence: 1 MSSPRKVRGKTGRDNDDEEG.....DIMNIVTMRKQRCGMQTK 405

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTDUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	28.0	2465	2	US-08-596-291-3
2	597	28.0	2465	3	US-09-100-804-3
3	597	28.0	2466	3	US-09-080-855-12
4	597	28.0	2466	4	US-09-566-076-12
5	597	28.0	2466	5	PCT-US94-09943-2
6	597	28.0	2485	3	US-09-290-640-46
7	597	28.0	2485	4	US-09-665-615B-46
8	474	22.2	913	4	US-09-848-294-2
9	466.5	21.9	278	1	US-08-201-697-16
10	462	21.7	231	2	US-08-446-345-37
11	462	21.7	244	4	US-09-848-294-7
12	456	21.4	242	2	US-08-683-982-21
13	456	21.4	242	2	US-09-144-925-21
14	455	21.3	1337	3	US-08-854-585-2
15	455	21.3	1337	4	US-09-447-533-2
16	455	21.3	1337	5	PCT-US95-05512-2
17	445	20.9	1174	2	US-08-446-345-36
18	440.5	20.7	1501	2	US-08-447-464-3
19	440.5	20.7	1501	2	US-08-716-679-3
20	439.5	20.6	232	2	US-08-448-345-38
21	439.5	20.6	1911	1	US-08-348-006B-5
22	439.5	20.6	1911	2	US-08-800-825A-5
23	439.5	20.6	1911	3	US-09-158-657-5
24	439.5	20.6	1911	5	PCT-US94-10166-5
25	436	20.4	1188	1	US-08-201-697-4
26	435	20.4	1439	2	US-08-449-644-2
27	435	20.4	1439	2	US-08-087-244A-2

28	435	20.4	2314	4	US-09-816-703A-2	Sequence 2, Appli
29	434	20.3	1452	2	US-08-449-644-8	Sequence 8, Appli
30	434	20.3	1452	2	US-08-087-244A-8	Sequence 8, Appli
31	434	20.3	1457	2	US-08-652-971-3	Sequence 3, Appli
32	434	20.3	1457	2	US-08-449-644-1	Sequence 1, Appli
33	434	20.3	1457	2	US-08-087-244A-1	Sequence 3, Appli
34	434	20.3	1457	2	US-08-991-258A-3	Sequence 3, Appli
35	434	20.3	1457	2	US-08-769-399-3	Sequence 3, Appli
36	434	20.3	1457	3	US-08-991-953A-3	Sequence 9, Appli
37	432	20.3	246	4	US-09-848-294-9	Sequence 3, Appli
38	432	20.3	1187	1	US-08-201-697-2	Sequence 2, Appli
39	432	20.3	1452	2	US-08-652-971-4	Sequence 4, Appli
40	432	20.3	1452	2	US-08-991-258A-4	Sequence 4, Appli
41	432	20.3	1452	2	US-08-769-399-4	Sequence 4, Appli
42	432	20.3	1452	3	US-08-991-953A-4	Sequence 4, Appli
43	431.5	20.2	254	2	US-08-685-992-14	Sequence 14, Appli
44	431.5	20.2	254	2	US-09-144-925-14	Sequence 14, Appli
45	431.5	20.2	2308	1	US-08-015-973-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-596-291-3

; Sequence 3, Application US/08596291

; Patent No. 5821075

; GENERAL INFORMATION:

; APPLICANT: GOMEZ, LEONEL JORGE

; APPLICANT: SARAS, JAN

; APPLICANT: CLAESSON-WELSH, LENA

; APPLICANT: HELDIN, CARL-HENRIK

; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

; TITLE OF INVENTION: TYROSINE PHOSPHATASES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/596,291

; FILING DATE: 09-AUG-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/115,573

; FILING DATE: 01-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: GATES, EDWARD R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: LO461/7000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; TELEX: 92-1742 EZEKIEL

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2465 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-596-291-3

Query Match 28.0%; Score 597; DB 2; Length 2465;  
Best Local Similarity 33.8%; Pred. No. 3.5e-48;





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QY 6 KVRKGTGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGNKNNSNVKPSHHLSF 62
DB 2070 KMGKLSERTEDTDCG-----SPLPEYFTEATKMGCEYCEEKVKSLSL-----2116
QY 63 SDKYELVYPPLESDDTETVMDVSDRLNRWNSMSETAGPSKTVSPVLSSGSRSLSKDT 122
DB 2117 -----IQKPEKKTDDDEITWG-NDELPFERTNHEDSD-----KD-2150
QY 123 ETSVSEKELTOLAQIRPLIENSSARSAMRCLNTLQ-----KKEELDIIRREFLEBQM 175
DB 2151 HSFLTNDELAVLPVVKVLPSPGKYTGANLKSIVIRGLDQGPISKELENLQELKPLDQC 2210
QY 176 TLPDDFNSGNTLQNRDQRYRDLIPYDSTRVPLGKNGKYNASIRIVNHEEYFYIATQ 235
DB 2211 LI-----GQTKENRRKRYKNILPYDATRVPLGDEGGYINASFIKIPVKGEEFYIACQ 2264
QY 236 GLPETIEDFWQVLNNCNVIAITREIECGVIKCYSWPISL-KEPPEFEHFSVFLET 294
DB 2265 GLPFTTVGDFWQMLWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRRLALVR 2324
QY 295 FHTQYFTVRVFOIVKXSTGKSCVXHLQFTKWPDRHGTPTASADFFIKYVYVRKSHITGP 354
DB 2325 MQQLKGFVVRAMTLEDIQTRVHRHSHLNFTAWPDHDTSPQDDELTFISYMRHHSRGP 2384
QY 355 LLVHCSAGVGRGTGVFCVDVWFSAIKNYSFDIMNIVTQMRKQRCGMIOTK 405
DB 2385 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTE 2435

RESULT 4
US-09-566-076-12
; Sequence 12, Application US/09566076
; Patent No. 6475775
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzen, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heidlin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; EARLIER APPLICATION NUMBER: 09/080,855
; EARLIER FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-566-076-12

Query Match 28.0%; Score 597; DB 4; Length 2466;
Best Local Similarity 33.8%; Pred. No. 3.5e-48;
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;

QY 6 KVRKGTGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGNKNNSNVKPSHHLSF 62
DB 2070 KMGKLSERTEDTDCG-----SPLPEYFTEATKMGCEYCEEKVKSLSL-----2116
QY 63 SDKYELVYPPLESDDTETVMDVSDRLNRWNSMSETAGPSKTVSPVLSSGSRSLSKDT 122
DB 2117 -----IQKPEKKTDDDEITWG-NDELPFERTNHEDSD-----KD-2150
QY 123 ETSVSEKELTOLAQIRPLIENSSARSAMRCLNTLQ-----KKEELDIIRREFLEBQM 175
DB 2151 HSFLTNDELAVLPVVKVLPSPGKYTGANLKSIVIRGLDQGPISKELENLQELKPLDQC 2210
QY 176 TLPDDFNSGNTLQNRDQRYRDLIPYDSTRVPLGKNGKYNASIRIVNHEEYFYIATQ 235
DB 2211 LI-----GQTKENRRKRYKNILPYDATRVPLGDEGGYINASFIKIPVKGEEFYIACQ 2264
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QY 236 GLPETIEDFWQVLNNCNVIAITREIECGVIKCYSWPISL-KEPPEFEHFSVFLET 294
DB 2265 GLPFTTVGDFWQMLWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRRLALVR 2324
QY 295 FHTQYFTVRVFOIVKXSTGKSCVXHLQFTKWPDRHGTPTASADFFIKYVYVRKSHITGP 354
DB 2325 MQQLKGFVVRAMTLEDIQTRVHRHSHLNFTAWPDHDTSPQDDELTFISYMRHHSRGP 2384
QY 355 LLVHCSAGVGRGTGVFCVDVWFSAIKNYSFDIMNIVTQMRKQRCGMIOTK 405
DB 2385 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTE 2435

RESULT 5
PCT-US94-09943-2
; Sequence 2, Application PC/TUS9409943
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY, MICHAEL J.
; REGISTRATION NUMBER: P-38,349
; REFERENCE/DOCKET NUMBER: L0461/7000WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZEKIEL
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-09943-2

Query Match 28.0%; Score 597; DB 5; Length 2466;
Best Local Similarity 33.8%; Pred. No. 3.5e-48;
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;

QY 6 KVRKGTGRDNDEEGNSGNLNLNSLP---SSSQKMTPTKPIFGNKNNSNVKPSHHLSF 62
DB 2070 KMGKLSERTEDTDCG-----SPLPEYFTEATKMGCEYCEEKVKSLSL-----2116
QY 63 SDKYELVYPPLESDDTETVMDVSDRLNRWNSMSETAGPSKTVSPVLSSGSRSLSKDT 122
DB 2117 -----IQKPEKKTDDDEITWG-NDELPFERTNHEDSD-----KD-2150
QY 123 ETSVSEKELTOLAQIRPLIENSSARSAMRCLNTLQ-----KKEELDIIRREFLEBQM 175
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DB 2151 HSFITNDELAVLPVVKVLPSCGYTGANKLKVIRVIRGLDQGGIPSKELNQLKPLDQC 2210  
QY 176 TLPPDFNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKYINASVIRVNHHEEYFYIATQ 235  
DB 2211 LI-----GQTKENRRKRYKNILPYDATRVPLDGGYINAFIKIPVKGEEFYIACQ 2264  
QY 236 GLPPTIEDFQWVLNKNVNIAMITREIECGVTKCYSPISL-KEPLEFHFVSFLET 294  
DB 2265 GLPPTTVDGFWQMIWEQKSTVIAMTQVEGEKIKCQRYWNLGKTVMVSNRLALVR 2324  
QY 295 FHVTQYFTRVFOIVKSTGKSCVXHLQFTKMPDHGTIPASADFFIKYVRYVRKSHITGP 354  
DB 2325 MQQLKGFVVRAMTLEDIQTRVVRHISHLNFTAMPDHTPSQPDLLTFISYMRHHRSGP 2384  
QY 355 LLVHCSAGVGRGTGVFICVDVWVFSIAEKNSYFDIMNIVTQMRKQRCGMIOTK 405  
DB 2385 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRQMLQHRGVQTE 2454

## RESULT 6

US-09-290-640-46  
; Sequence 46, Application US/09290640  
; Patent No. 6204055  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-0351  
; CURRENT APPLICATION NUMBER: US/09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 2485  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-290-640-46

Query Match 28.0%; Score 597; DB 3; Length 2485;  
Best Local Similarity 33.8%; Pred. No. 3.5e-48;  
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;  
QY 6 KVRGKTGRNDEEGNSGNLNRSLP---SSSQMTPTKPIFGNKNNSNVKPSHLSF 62  
DB 2089 KMGKLSSEERTEDTDCG-----SPLPYFTATKNGCEEYCEBKVKSESL----- 2135  
QY 63 SKYELVYPEPLESDTDETVWDVDSRLNRWNSWDSETAGPSKTVSPVLSGSSRLSKDT 122  
DB 2136 -----IQKPEKKTDDDELITWG-NDELPIERTNHEDSD-----KD- 2169  
QY 123 ETSVSEKELTQLAQIRPLIFNSSASAMRDCLNTLQ-----KKELDIIRFPLEEQM 175  
DB 2170 HSFLTNDELAVLPVVKVLPSCGYTGANKLKVIRVIRGLDQGGIPSKELNQLKPLDQC 2229  
QY 176 TLPPDFNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKYINASVIRVNHHEEYFYIATQ 235  
DB 2230 LI-----GQTKENRRKRYKNILPYDAIRVPLDGGYINAFIKIPVKGEEFYIACQ 2283  
QY 236 GLPPTIEDFQWVLNKNVNIAMITREIECGVTKCYSPISL-KEPLEFHFVSFLET 294  
DB 2284 GLPPTTVDGFWQMIWEQKSTVIAMTQVEGEKIKCQRYWNLGKTVMVSNRLALVR 2343  
QY 295 FHVTQYFTRVFOIVKSTGKSCVXHLQFTKMPDHGTIPASADFFIKYVRYVRKSHITGP 354  
DB 2344 MQQLKGFVVRAMTLEDIQTRVVRHISHLNFTAMPDHTPSQPDLLTFISYMRHHRSGP 2403  
QY 355 LLVHCSAGVGRGTGVFICVDVWVFSIAEKNSYFDIMNIVTQMRKQRCGMIOTK 405  
DB 2404 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRQMLQHRGVQTE 2454

## RESULT 7

US-09-290-640-46

US-09-665-615B-46  
; Sequence 46, Application US/09665615B  
; Patent No. 6653133  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-0502  
; CURRENT APPLICATION NUMBER: US/09/665,615B  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/290,640  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 2485  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-665-615B-46

Query Match 28.0%; Score 597; DB 4; Length 2485;  
Best Local Similarity 33.8%; Pred. No. 3.5e-48;  
Matches 139; Conservative 69; Mismatches 147; Indels 56; Gaps 9;  
QY 6 KVRGKTGRNDEEGNSGNLNRSLP---SSSQMTPTKPIFGNKNNSNVKPSHLSF 62  
DB 2089 KMGKLSSEERTEDTDCG-----SPLPYFTATKNGCEEYCEBKVKSESL----- 2135  
QY 63 SKYELVYPEPLESDTDETVWDVDSRLNRWNSWDSETAGPSKTVSPVLSGSSRLSKDT 122  
DB 2136 -----IQKPEKKTDDDELITWG-NDELPIERTNHEDSD-----KD- 2169  
QY 123 ETSVSEKELTQLAQIRPLIFNSSASAMRDCLNTLQ-----KKELDIIRFPLEEQM 175  
DB 2170 HSFLTNDELAVLPVVKVLPSCGYTGANKLKVIRVIRGLDQGGIPSKELNQLKPLDQC 2229  
QY 176 TLPPDFNSGNTLQNRDKRYRDLIPYDSTRVPLGKNKYINASVIRVNHHEEYFYIATQ 235  
DB 2230 LI-----GQTKENRRKRYKNILPYDAIRVPLDGGYINAFIKIPVKGEEFYIACQ 2283  
QY 236 GLPPTIEDFQWVLNKNVNIAMITREIECGVTKCYSPISL-KEPLEFHFVSFLET 294  
DB 2284 GLPPTTVDGFWQMIWEQKSTVIAMTQVEGEKIKCQRYWNLGKTVMVSNRLALVR 2343  
QY 295 FHVTQYFTRVFOIVKSTGKSCVXHLQFTKMPDHGTIPASADFFIKYVRYVRKSHITGP 354  
DB 2344 MQQLKGFVVRAMTLEDIQTRVVRHISHLNFTAMPDHTPSQPDLLTFISYMRHHRSGP 2403  
QY 355 LLVHCSAGVGRGTGVFICVDVWVFSIAEKNSYFDIMNIVTQMRKQRCGMIOTK 405  
DB 2404 IITHCSAGIGRSGTLICIDVVLGLISQDLDFDISDLVRQMLQHRGVQTE 2454

## RESULT 8

US-09-848-294-2  
; Sequence 2, Application US/09848294  
; Patent No. 6479640  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas K.  
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el  
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
; TITLE OF INVENTION: Adhesions and Uses Therefor  
; FILE REFERENCE: CSHL90-04FZA  
; CURRENT APPLICATION NUMBER: US/09/848,294  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 09/235,251  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 08/759,536  
; PRIOR FILING DATE: 1996-12-04  
; PRIOR APPLICATION NUMBER: 08/107,420  
; PRIOR FILING DATE: 1993-08-16  
; PRIOR APPLICATION NUMBER: 07/663,579

; PRIOR FILING DATE: 1991-03-01  
; PRIOR APPLICATION NUMBER: 07/494,036  
; PRIOR FILING DATE: 1990-03-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 913  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-294-2

Query Match 22.2%; Score 474; DB 4; Length 913;  
Best Local Similarity 32.1%; Pred. No. 6.28-37;  
Matches 134; Conservative 60; Mismatches 156; Indels 68; Gaps 15;  
QY 13 RNDDEEGNGNLNRLNSPLSSQKMTPTKPIFGNKNSENKVPK--HHLFSKDKVELVY 70  
DB 512 RITPDGKFG-FNLKGGV---DQKM---PLVVSRLNPSPADTCIPKLNESQIVLIN 563  
QY 71 PPPLSDTDTETWVDSRLNRNNSMSETAGSKTVSPVLSSRLSKDTSTVSSEKE 130  
DB 564 GRDISETHDQV-----VNFKASRSHSRSLALVIRRAVRSPADFKSEDE 610  
QY 131 LQLAQIRPLFNSSARGAMRDCL--NTLQKKELDIIRFLELEQW-----T 176  
DB 611 LNLQ--FPEAIFPMCEGG--DTLEGMAQLKKGLESSTVLQFQELYRKKPKGLAITPAK 666  
QY 177 LPDDFNSGNTLQNRKNRYRDLPLVDSTVPLGKQKDYINASVI-----RIVNHEEY 229  
DB 667 LP-----QNLQKRYKQVLPYDTTRVLQGNEDYINASYNNMEIPAANLVNK---- 713  
QY 230 FYIATQGGPLPETIEDFWQWVLENNCNVIAMITREIEGVIKCYSYMPISLKEPFEH-- 287  
DB 714 -YIATQGGPLPHTCAQFWQVVDQKLSLIVLTLTTERGRTKCHQYWP---DPDVNNHGG 769  
QY 288 FSVFLETHVTQYFTRVRFQIVKSTGKSCQVCHLOFTKWPDEGTPASADFFIKYRYVR 347  
DB 770 FHIQCSDECTIAYVSREMLVTNTQTBEEHTVTHLQVAMPDGHGIPDSDSDFLEFVNYR 829  
QY 348 KSHI-TGPIILVHCSAGVGTGVFCVDFVFAIEKNTSFDIMNIVTQMRKQRCGM1QT 404  
DB 830 SLRVDSFVLVHCSAGIGRTGLVMTMETAMCLTERNLPVPLDVRKMRDQRAMVQT 887

RESULT 9  
US-08-201-697-16  
; Sequence 16, Application US/08201697  
; Patent No. 5785623  
; GENERAL INFORMATION:  
; APPLICANT: Wiggins, Roger C.  
; APPLICANT: Thomas, Feedikayil E.  
; TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein  
; TITLE OF INVENTION: 1  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/201,697  
; FILING DATE: 25-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-UM 9783  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 278 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-201-697-16

Query Match 21.9%; Score 466.5; DB 1; Length 278;  
Best Local Similarity 39.8%; Pred. No. 4.9e-37;  
Matches 103; Conservative 44; Mismatches 99; Indels 13; Gaps 5;  
QY 157 LQKKELDIIRFLELEQWTLPEDFNSGNTLQNRKNRYRDLPLVDSTVPLGK-----N 211  
DB 14 LQADSNTLLSKVEELKDVGRNQSCDIALLPENGRKNRYNNILPYDATRVKLSNVDDPPC 73  
QY 212 KDYNASIRIVNHEEYFYIATQGGPLPETIEDFWQWVLENNCNVIAMITREIEGVIK 271  
DB 74 SDYNASYIPGNFRF--YIVTQGGPLGKDDFWKQWQVQNVHNVMTQCVKGRVKC 131  
QY 272 YSWPISLKEPFEHFSVLETFHTVTVTRVQIV-KKSTGKSCQVCHLOFTKWPDPH 330  
DB 132 DHYWPAQ-QDSLIVYGDLLQLMLSESVLPETWITREFKIQGEEQLDAHRLIRHFTVWPDH 190  
QY 331 GTPASADFFIKYR-----YVRKSHITGPIILVHCSAGVGTGVFCVDFVFAIEKNTSFD 386  
DB 191 GVETTSQSLQFVTRVDYINRSPGAGTVVHCSAGVGTGVTFIALDRILQQLDSKDSVD 250  
QY 387 IMNIVTQMRKQRCGM1QTK 405  
DB 251 IFGIIVAMRKERYVMVQTE 269

RESULT 10  
US-08-446-345-37  
; Sequence 37, Application US/08446345  
; Patent No. 5831009  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Moller, Niels P.H.  
; APPLICANT: Moller, Karin B.  
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASES PTP-D1  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: N.Y.  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,345  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/234,440  
; FILING DATE: 28-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30742  
; REFERENCE/DOCKET NUMBER: 7683-054  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864



Db 178 VLVHCSAGIGRTGVLVMTAKCLTERNLPIYPLDIVRKMQRAMVQT 227

## RESULT 13

US-09-144-925-21

Sequence 21, Application US/09144925

Patent No. 5951979

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flinn, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02421-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,925

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,992

FILING DATE: July 25, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03Z

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-144-925-21

## Query Match

Best Local Similarity 41.74; Score 456; DB 2; Length 242;

Matches 96; Conservative 35; Mismatches 73; Indels 26; Gaps 7;

Y 188 QNRDKRYRDLPYDSRVLGKKNKOVINASYI-----RIVNHEEYFYIATQGLPE 240

Y 11 QLRDKRYKVLPTDTRVLQGNEDIVINASYINMEIPANLVNK-----YIATQGLPH 65

Y 241 TIEDFWQVLENNCNVIAMITREICGVKCYSWPISLKEPLFEHFSVLFETHV--- 297

Y 66 TCAQFWQVWDQKLSLIVMLTLTILGRKTKCHQWP---DPPDWMHGG-----FHIQCC 117

Y 298 TOYFTVAVFQ--IVKSTGSKQCVKHLQFTKWDHGTPTASADFFIKYVYVYKSHI--TCP 354

Y 118 SEDCTIAYVSLVNTGTGEEHTVTHLQVYVAVPDHGPDDSDFLFVFNYSRLRVSDSEP 177

Y 355 LLVHCSAGVGRGVFICVDVVFSAIKKNYSFDIMNIVTQMRKQRCGMQIQT 404

Y 178 VLVHCSAGIGRTGVLVMTAKCLTERNLPIYPLDIVRKMQRAMVQT 227

## RESULT 14

US-08-854-585-2

Sequence 2, Application US/08854585

Patent No. 6114140

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K. and stman, Arne

TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, Suite 6300

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,585

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/237,940

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1337 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-854-585-2

## Query Match

21.38; Score 455; DB 3; Length 1337;

Best Local Similarity 35.14; Pred. No. 8e-35;

Matches 105; Conservative 56; Mismatches 110; Indels 28; Gaps 8;

QY 119 SKDTETSVSEKELTQLAQIRPLIFNSSARSAMDCLNTLQKBEID----IIRFPLELEQ 174

Db 1003 AKNEVSFS-----QIKP-----KSKLIRVENPEAYFKQKQADSNCGFAEYEDLKL 1050

QY 175 MFLPDDFNSGNTLQNRDKRYRDLIPYDSTRVPLG-----KNKDYINASYIRIVNHEEYF 230

Db 1051 VGISQPKYAAALAEANRGKNRYNNVLPYDISRVKLSVQTHSTDDYINANTYMPGVHKKD-- 1108

QY 231 YIATQGLPETIEDFWQVLENNCNVIAMITREICGVKCYSWPISLKEPLFEHFSV 290

Db 1109 FIATQGLPLENTLXDFWQVWEKNVYAIIMLTCKVEQGRTKCEYWP--SKQADYGDITV 1166

QY 291 FLEFHTVQVTVRVFOIVKKGKQCVKHLQFTKWDHGTPTASADFFIKY---VR-YV 346

Db 1167 AMTSEIYLPENTIRDETFTKNIQTSESHPLRQFHTSPDHGVPDITDILLINFRYLVDYM 1226

QY 347 RKSHITGFLAVHCSAGVGRGVFICVDVVFSAIKKNYSFDIMNIVTQMRKQRCGMQIQT 405

Db 1227 KQSPPEPILVHCSAGVGRGVTFIADRLIYQIENENTVDYIGIVYDLRHRPLAVQTE 1285

## RESULT 15

US-09-447-533-2

Sequence 2, Application US/09447533

Patent No. 6552169

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

Ostman, Arne

TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE

PHOSPHATASES

NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Seed IP Law Group PLLC  
;; STREET: Suite 6300, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 980104  
;;  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/447,533  
;; FILING DATE: 23-No. 6592169-1999  
;; CLASSIFICATION: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Rosenman Ph.D., Stephen J.  
;; REGISTRATION NUMBER: 43,058  
;; REFERENCE/DOCKET NUMBER: 200125.402C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;;  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1337 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-447-533-2

Query Match 21.3%; Score 455; DB 4; Length 1337;  
Best Local Similarity 35.1%; Pred. No. 8e-35;  
Matches 105; Conservative 56; Mismatches 110; Indels 28; Gaps 8;

QY 119 SKDTETSVSEKLTQLAQIRPLIFNSSARSAMDCLNTLQKKELD----IIRFLELEQ 174  
DB 1003 AKNEVFSF-----QIRP-----KSKLIRVENFEAYFKQQAADNCGFAEEYEDLKL 1050  
QY 175 MTLPDFNSGNTLQNRKRYRDLPYDSTRVPLG----KNKDYINASYIRIVNHEEYFP 230  
DB 1051 VGISQPKYAAELAEENRGKRYNNVLPYDISKVKLSVQTHSTDDYINANTMPGVHSHKD-- 1108  
QY 231 YIATGPLEPTEIDPQWVLENNCNVIAITREICGVKCYSYMPISLKEPLEFEHFSV 290  
DB 1109 FIATGPLEPNTLKDFWRWWEKXNVYALIMLTCKVEQGRKCEYWP--SKQAQDYGDITV 1166  
QY 291 FLETHTVQYFTRVFOIVKKGKSCQVKHLQFTKMPDQGTGPASADFFIKY---VR-YV 346  
DB 1167 AMTSEIVLPWTIRDFVKNITQISESHPLRQPHFTSWPDHGVPTDTLLINRYLVRDYM 1226  
QY 347 RKSHITGPLLVHCSAGVGRGVFCVDVVFSALEKNYSEDIIMNVTOMKQKCGMIQTK 405  
DB 1227 KOSPPSPILVHCSAGVGRGTGTFIAIDRLIYQIENENTVDVYGVIVYDLRNRHPLMVQTE 1285

Search completed: June 21, 2004, 17:18:23  
Job time : 31 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 17:16:44 ; Search time 21 Seconds  
(without alignments)  
1855.122 Million cell updates/sec

Title: US-09-095-478A-7

Perfect score: 405

Sequence: 1 MSSPRKVRGKTGRNDEBEG.....DIMNIVTQMKQRCGMIOYK 405

Scoring table: OLIGO  
Gapop 60.0 ; Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

PIR 78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	19	4.7	398	2 T08716	protein-tyrosine-p
2	15	3.7	1174	2 T38140	protein-tyrosine-p
3	15	3.7	1175	2 S51005	protein-tyrosine-p
4	15	3.7	1176	2 T58315	protein-tyrosine-p
5	14	3.5	582	2 A57088	protein-tyrosine-p
6	14	3.5	1231	2 S53089	protein-tyrosine-p
7	14	3.5	1290	2 A56493	protein-tyrosine-p
8	14	3.5	1496	1 A48758	leukocyte common a
9	14	3.5	1499	2 T50212	protein-tyrosine-p
10	14	3.5	1501	2 T58148	protein-tyrosine-p
11	14	3.5	1691	1 D54689	protein-tyrosine-p
12	14	3.5	1863	2 S46217	protein-tyrosine-p
13	14	3.5	1894	2 C54689	protein-tyrosine-p
14	14	3.5	1897	1 TDHULX	protein-tyrosine-p
15	14	3.5	1898	2 S46216	leukocyte antigen-
16	14	3.5	1907	2 S50893	protein-tyrosine-p
17	14	3.5	1912	2 A56178	protein-tyrosine-p
18	14	3.5	2051	2 T30938	receptor tyrosine
19	14	3.5	2302	2 T14328	protein-tyrosine-p
20	12	3.0	184	2 T15125	hypothetical prote
21	12	3.0	1187	1 JC4155	protein-tyrosine-p
22	12	3.0	1189	1 JC2366	protein-tyrosine-p
23	12	3.0	1217	2 T22672	hypothetical prote
24	12	3.0	1238	2 S68700	HPTP beta-like tyr
25	12	3.0	1337	1 T38670	protein-tyrosine-p
26	12	3.0	1442	1 A48148	protein-tyrosine-p
27	12	3.0	1445	1 A48148	protein-tyrosine-p
28	12	3.0	1462	1 B36182	protein-tyrosine-p
29	12	3.0	1711	1 A55148	protein-tyrosine-p

30	11	2.7	198	2 T27722	hypothetical prote
31	11	2.7	256	2 A40169	protein-tyrosine-p
32	11	2.7	335	1 A39862	protein-tyrosine-p
33	11	2.7	398	2 I56540	protein-tyrosine-p
34	11	2.7	405	2 I49372	protein-tyrosine-p
35	11	2.7	405	2 S68250	protein-tyrosine-p
36	11	2.7	483	2 T25992	hypothetical prote
37	11	2.7	521	1 A44267	protein-tyrosine-p
38	11	2.7	550	1 A40449	protein-tyrosine-p
39	11	2.7	583	2 S17671	protein-tyrosine-p
40	11	2.7	699	2 JC6132	protein-tyrosine-p
41	11	2.7	700	1 S12053	protein-tyrosine-p
42	11	2.7	711	1 S28351	protein-tyrosine-p
43	11	2.7	796	1 JC1285	protein-tyrosine-p
44	11	2.7	802	1 A36065	protein-tyrosine-p
45	11	2.7	829	1 A49734	protein-tyrosine-p
46	11	2.7	1118	1 A49724	protein-tyrosine-p
47	11	2.7	1187	1 A53661	protein-tyrosine-p
48	11	2.7	1188	1 A57064	protein-tyrosine-p
49	11	2.7	1200	2 T43148	probable protein-t
50	11	2.7	1216	2 S60613	protein-tyrosine-p
51	11	2.7	1226	2 JC7503	protein-tyrosine-p
52	11	2.7	1237	2 A54080	protein-tyrosine-p
53	11	2.7	1262	1 B48758	protein-tyrosine-p
54	11	2.7	1273	1 TDRILT	leukocyte common a
55	11	2.7	1291	1 A28334	protein-tyrosine-p
56	11	2.7	1301	1 A41622	protein-tyrosine-p
57	11	2.7	1304	1 A46546	leukocyte common a
58	11	2.7	1422	2 T42636	protein-tyrosine-p
59	11	2.7	1437	2 T31093	probable protein-t
60	11	2.7	1585	2 T19121	protein-tyrosine-p
61	11	2.7	1997	1 S12050	protein-tyrosine-p
62	11	2.7	2029	1 TDFPLK	protein-tyrosine-p
63	11	2.7	2314	1 A46151	protein-tyrosine-p
64	10	2.5	166	2 T34229	hypothetical prote
65	10	2.5	490	2 T21365	hypothetical prote
66	10	2.5	490	2 T25430	hypothetical prote
67	10	2.5	518	2 T29589	hypothetical prote
68	10	2.5	650	2 B47791	protein B0207.1 (i
69	10	2.5	1409	2 T42522	protein-tyrosine-p
70	9	2.2	108	2 S51687	protein-tyrosine-p
71	9	2.2	130	2 T29155	hypothetical prote
72	9	2.2	248	2 T46903	hypothetical prote
73	9	2.2	374	2 T29154	hypothetical prote
74	9	2.2	405	2 A33939	Fc gamma (IgG) rec
75	9	2.2	597	2 B53978	protein-tyrosine-p
76	9	2.2	694	2 A53978	protein-tyrosine-p
77	9	2.2	750	2 S67100	protein-tyrosine-p
78	9	2.2	913	1 A41109	protein-tyrosine-p
79	9	2.2	1015	2 JC5263	transmembrane tyro
80	9	2.2	1015	2 JC5062	phogrin precursor
81	9	2.2	1156	2 T23308	hypothetical prote
82	9	2.2	1367	2 T21913	hypothetical prote
83	9	2.2	1557	2 B41214	protein-tyrosine-p
84	9	2.2	1615	2 B49502	protein-tyrosine-p
85	9	2.2	1630	2 C41214	protein-tyrosine-p
86	9	2.2	1767	2 A49502	protein-tyrosine-p
87	8	2.0	69	2 PS0368	protein-tyrosine-p
88	8	2.0	340	2 T51846	protein-tyrosine-p
89	8	2.0	340	2 C96741	hypothetical prote
90	8	2.0	548	1 T37577	islet cell antigen
91	8	2.0	550	2 T32543	hypothetical prote
92	8	2.0	573	2 A33533	cell surface glyco
93	8	2.0	711	2 T45160	protein-tyrosine-p
94	8	2.0	802	1 B44390	protein-tyrosine-p
95	8	2.0	922	1 S54342	protein-tyrosine-p
96	8	2.0	979	1 JC2349	protein-tyrosine-p
97	8	2.0	996	2 I48721	PYP 35 protein - m
98	8	2.0	1422	2 T30111	hypothetical prote
99	7	1.7	35	2 PS0363	protein-tyrosine-p
100	7	1.7	35	2 PS0364	protein-tyrosine-p



## ALIGNMENTS

## RESULT 1

T08716

protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999

C/Accession: T08716

R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16472

A/Accession: T08716

A:Molecule type: mRNA

A:Residues: 1-398 &lt;ANS&gt;

A/Cross-references: EMBL:AL050040

A/Experimental source: fetal kidney; clone DKFZp566K0524

C:Genetics: &lt;PTP&gt;

A&gt;Note: DKFZp566K0524.1

C/Superfamily: protein-tyrosine-phosphatase homology

F:161-379/Domain: protein-tyrosine-phosphatase homology &lt;PTP&gt;

Query Match

Best Local Similarity 4.7%; Score 19; DB 2; Length 398;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KRYRDILPYDSTRVPLGK 210

|||||

DB 164 KRYRDILPYDSTRVPLGK 182

## RESULT 2

I38140

protein-tyrosine-phosphatase (EC 3.1.3.48) - human

C:Species: Homo sapiens (man)

C&gt;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 22-Jun-1999

C/Accession: I38140

R:Moller, N.P.; Moller, K.B.; Lammers, R.; Kharitonkov, A.; Sures, I.; Ullrich, A.

Proc. Natl. Acad. Sci. U.S.A. 91, 7477-7481, 1994

A&gt;Title: Src kinase associates with a member of a distinct subfamily of protein-tyrosine

A/Reference number: I38140; MUID:94329538; PMID:7519780

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1174 &lt;RES&gt;

A/Cross-references: EMBL:X79510; NID:G532055; PIDN:CA856042.1; PID:G532056

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:25-304/Domain: protein 4.1 membrane-binding domain homology &lt;B41&gt;

F:921-1156/Domain: protein-tyrosine-phosphatase homology &lt;PTP2&gt;

F:1109/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1114/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 3.7%; Score 15; DB 2; Length 1174;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGTGV 368

|||||

DB 1103 PLLVHCSAGVGRGTGV 1117

## RESULT 3

S51005

protein-tyrosine-phosphatase (EC 3.1.3.48) 2E - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 10-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999

C/Accession: S51005; S51161

R:U'Abbe, D.; Barville, D.; Tong, Y.; Stocco, R.; Masson, S.; Ma, S.; Fantus, G.; Shen,

FEBS Lett. 356, 331-356, 1994

A&gt;Title: Identification of a novel protein tyrosine phosphatase with sequence homology b

A/Reference number: S51005; MUID:95104449; PMID:7805871

A/Accession: S51005

A:Molecule type: mRNA

A:Residues: 1-1175 &lt;LAB&gt;

A/Cross-references: EMBL:U17971; NID:G662113; PIDN:AAA62153.1; PID:G602255

A/Genetics: PTP2E

A/Accession: S51161

A:Molecule type: mRNA

A:Residues: 840-1175 &lt;LAB&gt;

A/Cross-references: EMBL:U18293; NID:G603228; PIDN:AAA62154.1; PID:G603229

A/Genetics: PTP2E1

C/Genetics: &lt;PTP2E&gt;

A/Note: clone PTP2E

A/Note: clone PTP2E1

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat

F:25-304/Domain: protein 4.1 membrane-binding domain homology &lt;B41&gt;

F:922-1157/Domain: protein-tyrosine-phosphatase homology &lt;PTP2&gt;

F:1109/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1115/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 3.7%; Score 15; DB 2; Length 1175;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGTGV 368

|||||

DB 1104 PLLVHCSAGVGRGTGV 1118

## RESULT 4

I58345

protein tyrosine phosphatase - mouse

C:Species: Mus musculus (house mouse)

C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 22-Jun-1999

C/Accession: I58345

R:Higashitsuji, H.; Arii, S.; Furutani, M.; Imamura, M.; Kaneko, Y.; Takenawa, J.; Nak

Oncogene 10, 407-414, 1995

A&gt;Title: Enhanced expression of multiple protein tyrosine phosphatases in the regenera

tal protein 4.1.

A/Reference number: I58345; MUID:95140431; PMID:7838537

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1176 &lt;RES&gt;

A/Cross-references: GB:D37801; NID:G604885; PIDN:BAA07053.1; PID:G604886

C/Genetics: &lt;PTP&gt;

A/Genes: PTP-RL10

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane

C/Keywords: phosphoprotein

F:25-304/Domain: protein 4.1 membrane-binding domain homology &lt;B41&gt;

F:923-1158/Domain: protein-tyrosine-phosphatase homology &lt;PTP2&gt;

F:1110/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1116/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 3.7%; Score 15; DB 2; Length 1176;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGTGV 368

|||||

DB 1105 PLLVHCSAGVGRGTGV 1119

## RESULT 5

A57068

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)

N/Alternate names: leukocyte antigen-related protein LAR

C:Species: Mus musculus (house mouse)

C/Date: 03-Oct-1995 #sequence\_revision 09-Mar-1996 #text\_change 23-Jul-1999

C/Accession: A57068; S40280

R:Schaaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Oide Weghuis, D

Genomics 27, 124-130, 1995

A&gt;Title: The mouse gene Ptpfr encoding the leukocyte common antigen-related molecule L

A:Reference number: A57068; MUID:95394448; PMID:7665159  
A:Accession: A57068  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-582 <SCH>  
A:Cross-references: GB:Z37988; NID:993005; PIDN:CAA86070.1; PID:g993006  
R:Heudriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
submitted to the EMBL Data Library, June 1993  
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
A:Reference number: S40280  
A:Accession: S40280  
A:Molecule type: mRNA  
A:Residues: 116-221 <HNR>  
A:Cross-references: EMBL:223049; NID:g438135; PIDN:CAA80584.1; PID:g438136  
C:Genetics:  
A:Gene: Ptpfr  
A:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
Ogy  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>  
F:50-271/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:339-562/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:223/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:229/Binding site: substrate phosphate (Arg) #status predicted  
F:514/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 582;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
|||||  
DB 512 VHCAGVGRGTGVFI 525  
|||||

RESULT 6  
S53089  
A:Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from th  
N:Alternate names: leukocyte antigen-related protein  
C:Species: Anopheles gambiae (African malaria mosquito)  
C>Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S53089  
R:Spier, S.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53089  
A:Accession: S53089  
A:Molecule type: DNA  
A:Residues: 1-1231 <SPI>  
C:Genetics:  
A:Cross-references: EMBL:X85217; NID:g732549; PIDN:CAA59483.1; PID:g732550  
A:Introns: 1026/3; 1070/3; 1209/3  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
Ogy  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:208-293/Domain: fibronectin type III repeat homology <3FR>  
F:619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:872/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1163/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1169/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1231;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
|||||  
DB 1161 VHCAGVGRGTGVFI 1174  
|||||

RESULT 7  
A56493  
Leukocyte common antigen-related protein (LAR) - rat (fragment)  
N:Alternate names: LAR receptor-linked tyrosine phosphatase  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C:Accession: A56493; I55393  
R:Zhang, J.S.; Longo, P.M.  
J. Cell Biol. 128:415-431, 1995  
A:Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the  
A:Reference number: A56493; MUID:95146548; PMID:7844155  
A:Accession: A56493  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1290 <RES>  
A:Cross-references: EMBL:X83505; NID:g732918; PIDN:CAA58495.1; PID:g732919  
R:Longo, P.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.  
J. Biol. Chem. 268:26503-26511, 1993  
A:Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulat  
A:Reference number: I55393; MUID:94075340; PMID:8253779  
A:Accession: I55393  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 831-1290 <RES2>  
A:Cross-references: EMBL:U00477; NID:g392565; PIDN:AA04306.1; PID:g392566  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
Ogy  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat  
F:80-166/Domain: fibronectin type III repeat homology <3FR>  
F:167-1290/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:931/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:937/Binding site: substrate phosphate (Arg) #status predicted  
F:1222/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1228/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1290;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
|||||  
DB 1220 VHCAGVGRGTGVFI 1233  
|||||

RESULT 8  
A48758  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48758  
R:Pan, M.G.; Kim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.  
J. Biol. Chem. 268:19284-19291, 1993  
A:Title: Cloning and expression of two structurally distinct receptor-linked protein-ty  
A:Reference number: A48758; MUID:93374907; PMID:8396131  
A:Accession: A48758  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1496 <PAN>  
A:Cross-references: GB:L19180  
A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as C  
as Phe  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
Ogy  
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; trans  
F:149-209/Domain: immunoglobulin homology <IMM1>  
F:246-300/Domain: immunoglobulin homology <IMM2>  
F:318-405/Domain: fibronectin type III repeat homology <FN3A>  
F:411-504/Domain: fibronectin type III repeat homology <FN3B>  
F:509-599/Domain: fibronectin type III repeat homology <FN3C>  
F:600-684/Domain: fibronectin type III repeat homology <FN3H>  
F:880-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>

P;1140/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F;1146/Binding site: substrate phosphate (Arg) #status predicted  
 F;1429/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F;1435/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 1; Length 1496;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGTGVFI 370

Db 1427 VHCAGVGTGVFI 1440

# RESULT 9

150212

protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1995 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000

A;Accession: I50212

R;Stoker, A.W. 46, 201-217, 1994

Mech. Dev. 46, 201-217, 1994

A;Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase

A;Reference number: I50212; MUID:95001563; PMID:7318104

A;Accession: I50212

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1499 <STO>

A;Cross-references: GB:L32780; NID:G485746; PIDN:AAA64460.1; PID:G485747

C;Genetic:

A;Gene: CYPALPHAL

C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

# ogv

F;148-208/Domain: immunoglobulin homology <IMM1>

F;245-299/Domain: immunoglobulin homology <IMM2>

F;317-399/Domain: fibronectin type III repeat homology <3FR>

F;881-1479/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F;1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;1141/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1147/Binding site: substrate phosphate (Arg) #status predicted

F;1432/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1438/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGTGVFI 370

Db 1430 VHCAGVGTGVFI 1443

# RESULT 10

158148

protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat

N;Alternate names: leukocyte common antigen-related phosphatase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 20-Jun-2000

C;Accession: I58148; S46218

R;Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.

Neuron 11, 387-400, 1993

A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen

A;Reference number: I58148; MUID:93357030; PMID:8352946

A;Accession: I58148

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1501 <WAL>

A;Cross-references: GB:L19933; NID:G310242; PIDN:AAA24203.1; PID:G310243

A;Note: in GenBank entry RATTYRPHOS, release 113.0, the source is designated as Rattus n

R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phd

A;Reference number: S46216; MUID:94347119; PMID:8068021

A;Accession: S46218

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-1501 <ZHA>

A;Cross-references: MID:G294573; PIDN:AAC37657.1; PID:G294574

C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology

ogv

C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyro

F;47-109/Domain: immunoglobulin homology <IMM1>

F;149-209/Domain: immunoglobulin homology <IMM2>

F;246-300/Domain: immunoglobulin homology <IMM3>

F;413-508/Domain: fibronectin type III repeat homology <3FR>

F;882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F;969-1130/Domain: protein-tyrosine-phosphatase homology <PTP1>

F;1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted

F;1149/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted

F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted

F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1501;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGTGVFI 370

Db 1431 VHCAGVGTGVFI 1444

# RESULT 11

DS4689

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precurs

N;Alternate names: MPTP delta type D

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: D54689; A54689

R;Wizum, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Mol. Cell. Biol. 13, 5513-5523, 1993

A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in speciali

A;Reference number: A54689; MUID:93360986; PMID:8355697

A;Accession: D54689

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1691 <MTZ>

A;Experimental source: brain

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIPI:136537)

A;Accession: A54689

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-398,799-1691 <MT2>

A;Experimental source: brain

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBIPI:136524)

C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology

ogv

C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester h

F;42-95/Domain: immunoglobulin homology <IMM3>

F;1075-1691/Domain: fibronectin type III repeat homology <PN3A>

F;1449-1671/Domain: protein-tyrosine-phosphatase homology <PTP2>

F;1333/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1339/Binding site: substrate phosphate (Arg) #status predicted

F;1623/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1629/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGTGVFI 370

Db 1621 VHCAGVGTGVFI 1634

RESULT 12

S46217

protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat

N/Alternate names: leukocyte common antigen-related phosphatase

C/Species: Rattus norvegicus (Norway rat)

C/Date: 07-May-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S46217; S51174; A9104

R/Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A/Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase

A/Reference number: S46216; MUID:94347119; PMID:8068021

A/Accession: S46217

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1863 <ZHA>

A/Cross-references: EMBL:L11587

R/Goldstein, B.J.

submitted to the EMBL Data Library, February 1993

A/Reference number: S51174

A/Accession: S51174

A/Molecule type: mRNA

A/Residues: 1-1788, 'G', 1790-1863 <GOL>

A/Cross-references: EMBL:L11587; MID:9205134; PIDN:RAC37656.1; PID:G205135

R/Yan, H.; Grossman, A.; Wang, H.; D'Austachio, P.; Mossie, K.; Musacchio, J.M.; Silvent

J. Biol. Chem. 268, 24880-24886, 1993

A/Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ne

A/Reference number: A49104; MUID:94043351; PMID:8227050

A/Accession: A49104

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>

A/Experimental source: brain

A/Note: sequence extracted from NCBI backbone (NCBIP:133669)

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy

C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F/1-26/Domain: signal sequence #status predicted <SIG>

F/27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>

F/149-209/Domain: immunoglobulin homology <IMM1>

F/246-300/Domain: immunoglobulin homology <IMM2>

F/318-400/Domain: fibronectin type III repeat homology <FN3A>

F/413-499/Domain: fibronectin type III repeat homology <FN3B>

F/511-592/Domain: fibronectin type III repeat homology <FN3C>

F/1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F/1331-1552/Domain: protein-tyrosine-phosphatase homology <PTP1>

F/1504/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1510/Binding site: substrate phosphate (Arg) #status predicted

F/1785/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1801/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1863;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 357 VHCAGVGTGVFI 370

Db 1793 VHCAGVGTGVFI 1806

RESULT 13

S54689

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor

N/Alternate names: MPTP delta type B/C

C/Contains: protein tyrosine phosphatase, receptor type delta, splice form C

C/Species: Mus musculus (house mouse)

C/Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 12-Feb-1999

C/Accession: S54689; B54689

R/Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Int. Cell. Biol. 13, 5513-5523, 1993

A/Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in speciali

A/Reference number: S54689; MUID:93360986; PMID:8355697

A/Accession: S54689

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1894 <Miz>

A/Experimental source: brain; splice form B

A/Note: sequence inconsistent with nucleotide translation

A/Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)

A/Accession: B54689

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MIZ>

A/Experimental source: brain; splice form C

A/Note: sequence inconsistent with nucleotide translation

A/Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology ogy

C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester h

F/45-107/Domain: immunoglobulin homology <IMM1>

F/245-299/Domain: immunoglobulin homology <IMM2>

F/317-399/Domain: fibronectin type III repeat homology <FN3A>

F/1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F/1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/1536/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1542/Binding site: substrate phosphate (Arg) #status predicted

F/1826/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1894;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370

Db 1824 VHCAGVGTGVFI 1837

RESULT 14

TDHULK

leukocyte antigen-related protein precursor - human

N/Alternate names: leukocyte common antigen homology

C/Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999

C/Accession: S03841; J10051

R/Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.

J. Exp. Med. 168, 1523-1530, 1988

A/Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region i

A/Reference number: J10051; MUID:89035978; PMID:2972752

A/Accession: S03841

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1897 <STR>

A/Cross-references: EMBL:Y00815; NID:G34266; PIDN:CAA68754.1; PID:G34267

C/Genetics:

A/Gene: GDB:PTPRF; LAR

A/Cross-references: GDB:120138; OMIM:179590

A/Map position: 1p34-1p34

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology ogy

C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembran

F/1-16/Domain: signal sequence #status predicted <SIG>

F/17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>

F/17-1250/Domain: extracellular #status predicted <EXT>

F/37-99/Domain: immunoglobulin homology <IMM1>

F/139-199/Domain: immunoglobulin homology <IMM2>

F/236-290/Domain: immunoglobulin homology <IMM3>

F/308-350/Domain: fibronectin type III repeat homology <FN3A>

F/403-489/Domain: fibronectin type III repeat homology <FN3B>

F/501-583/Domain: fibronectin type III repeat homology <FN3C>

F/596-685/Domain: fibronectin type III repeat homology <FN3D>

F/698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>

F:810-893/Domain: fibronectin type III repeat homology <FN3P>  
 F:905-989/Domain: fibronectin type III repeat homology <FN3G>  
 F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>  
 F:1251-1274/Domain: transmembrane #status predicted <INT>  
 F:1275-1897/Domain: intracellular #status predicted <INT>  
 F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1285-1897/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:44-97,146-197,243-288/Binding site: carbohydrate (Asn) #status predicted  
 F:107,240,285,711,956/Binding site: carbohydrate (Asn) #status predicted  
 F:1538/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1544/Binding site: substrate phosphate (Arg) #status predicted  
 F:1829/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 1; Length 1897;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1827 VHCAGVGRGTGVFI 1840

RESULT 15  
 S46216  
 Leukocyte antigen-related protein precursor - rat  
 N:Alternate names: leukocyte common antigen homolog  
 N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S46216; S23252; A41032; A33154  
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
 Biochem. J. 302, 39-47, 1994  
 A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase  
 A:Reference number: S46216; MUID:94347119; PMID:8068021  
 A:Accession: S46216  
 A:Status: nucleic acid sequence not shown  
 A:Residues: 1-1898 <ZEA>  
 A:Cross-references: EMBL:U11586; NID:G205132; PIDN:AAC37655.1; PID:G205133  
 R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
 Biochem. J. 284, 569-576, 1992  
 A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by threonine phosphatase  
 A:Reference number: S23252; MUID:92287069; PMID:1559438  
 A:Accession: S23252  
 A:Status: nucleic acid sequence not shown  
 A:Residues: 1-1604  
 A:Cross-references: EMBL:U11586; NID:G205132; PIDN:AAC37655.1; PID:G205133  
 R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
 Biochem. J. 284, 569-576, 1992  
 A:Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic domain of the insulin receptor  
 A:Reference number: A41032; MUID:92011772; PMID:1918076  
 A:Accession: A41032  
 A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
 A:Cross-references: GB:M60103; NID:G205130; PIDN:AAA41510.1; PID:G205131  
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
 submitted to the Protein Sequence Database, December 1990  
 A:Reference number: A33154  
 A:Accession: A33154  
 A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
 C:Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; t

F:318-400/Domain: fibronectin type III repeat homology <FN3A>  
 F:413-439/Domain: fibronectin type III repeat homology <FN3B>  
 F:511-533/Domain: fibronectin type III repeat homology <FN3C>  
 F:608-695/Domain: fibronectin type III repeat homology <FN3D>  
 F:708-799/Domain: fibronectin type III repeat homology <FN3E>  
 F:811-895/Domain: fibronectin type III repeat homology <FN3F>  
 F:906-990/Domain: fibronectin type III repeat homology <FN3G>  
 F:1002-1079/Domain: fibronectin type III repeat homology <FN3H>  
 F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TMM>  
 F:1276-1898/Domain: intracellular #status predicted <INT>  
 F:1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:54-107,156-207,253-298/Disulfide bonds: #status predicted  
 F:117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:1539/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1545/Binding site: substrate phosphate (Arg) #status predicted  
 F:1830/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1836/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1898;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1828 VHCAGVGRGTGVFI 1841

RESULT 16  
 S50893  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
 C:Accession: S50893; S40281  
 R:Wagner, J.; Boerboom, D.; Tremblay, M.L.  
 Eur. J. Biochem. 226, 773-782, 1994  
 A:Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-tyrosine phosphatase  
 A:Reference number: S50893; MUID:95112841; PMID:7529177  
 A:Accession: S50893  
 A:Status: preliminary  
 A:Residues: 1-1907 <WAG>  
 A:Cross-references: EMBL:X82288; NID:G587483; PIDN:CAA57732.1; PID:G587484  
 R:Handriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 A:Reference number: S40280  
 A:Accession: S40280  
 A:Residues: 1441-1501, 'E', 1503-1546 <HEN>  
 A:Cross-references: EMBL:Z23050; NID:G438137; PIDN:CAA80585.1; PID:G438138  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology  
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembran

Query Match 3.5%; Score 14; DB 2; Length 1907;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1837 VHCAGVGRGTGVFI 1850

## RESULT 17

A56178  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human  
 N:Alternate names: protein-tyrosine-phosphatase BPTP-2  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 21-Jan-2000  
 C:Accession: A56178; S12055; B44929  
 R:Fullido, R.; Krueger, N.X.; Serrano-Pages, C.; Saito, H.; Streuli, M.  
 J. Biol. Chem. 270, 6722-6728, 1995  
 A>Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.  
 A:Reference number: A56178; MUID:95204468; PMID:7896816  
 A:Accession: A56178  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1912 <FUL>  
 A:Cross-references: GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653  
 R:Krueger, N.X.; Streuli, M.; Saito, H.  
 EMBO J. 9, 3241-3252, 1990  
 A>Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases

A:Reference number: S12049; MUID:9106018; PMID:2170109  
 A:Accession: S12052  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 390-1912 <KRU>  
 A:Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790  
 A>Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T  
 R:Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Inai, K.; Yac  
 Cancer Res. 52, 737-740, 1992

A>Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.  
 A:Reference number: A44929; MUID:92119637; PMID:1370651  
 A:Accession: B44929  
 A:Molecule type: mRNA  
 A:Residues: 1756-1804 'C' 1806-1845 <ADA>  
 A:Cross-references: GB:S78886; NID:g745545; PIDN:AAB21147.1; PID:g743546  
 A:Experimental source: pre-B cell NALM-6  
 A>Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBI:P:78087)  
 A>Note: the authors did not report the entire codon for residue 90

C:Genetics:  
 A:Gene: GDB:PTPRD  
 A:Cross-references: GDB:131384; OMIM:601598  
 A:Map position: 9p24-9p24  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
 F:138-100/Domain: immunoglobulin homology <IMM1>  
 F:140-209/Domain: immunoglobulin homology <IMM2>  
 F:250-304/Domain: immunoglobulin homology <IMM3>  
 F:711-811/Domain: fibronectin type III repeat homology <3FR>  
 F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1553/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1559/Binding site: substrate phosphate (Arg) #status predicted  
 F:1844/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1912;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 1842 VHCAGVGRGTGVPI 1855

RESULT 18  
 T30938  
 receptor tyrosine phosphatase - medicinal leech  
 C:Species: Hirudo medicinalis (medicinal leech)  
 C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
 C:Accession: T30938

A:Reference number: A56178; MUID:95204468; PMID:7896816  
 A:Accession: A56178  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1912 <FUL>  
 A:Cross-references: GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653  
 R:Krueger, N.X.; Streuli, M.; Saito, H.  
 EMBO J. 9, 3241-3252, 1990  
 A>Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases

A:Reference number: S12049; MUID:9106018; PMID:2170109  
 A:Accession: S12052  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 390-1912 <KRU>  
 A:Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790  
 A>Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T  
 R:Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Inai, K.; Yac  
 Cancer Res. 52, 737-740, 1992

A>Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.  
 A:Reference number: A44929; MUID:92119637; PMID:1370651  
 A:Accession: B44929  
 A:Molecule type: mRNA  
 A:Residues: 1756-1804 'C' 1806-1845 <ADA>  
 A:Cross-references: GB:S78886; NID:g745545; PIDN:AAB21147.1; PID:g743546  
 A:Experimental source: pre-B cell NALM-6  
 A>Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBI:P:78087)  
 A>Note: the authors did not report the entire codon for residue 90

C:Genetics:  
 A:Gene: GDB:PTPRD  
 A:Cross-references: GDB:131384; OMIM:601598  
 A:Map position: 9p24-9p24  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
 F:138-100/Domain: immunoglobulin homology <IMM1>  
 F:140-209/Domain: immunoglobulin homology <IMM2>  
 F:250-304/Domain: immunoglobulin homology <IMM3>  
 F:711-811/Domain: fibronectin type III repeat homology <3FR>  
 F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:1553/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1559/Binding site: substrate phosphate (Arg) #status predicted  
 F:1844/Active site: Cys (phosphotyrosine intermediate) #status predicted  
 F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.5%; Score 14; DB 2; Length 1912;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 1842 VHCAGVGRGTGVPI 1855

RESULT 19  
 T14328  
 protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type, GMCI precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T14328  
 R:Wright, M.B.; Hugo, C.; Seifert, R.; Distech, C.M.; Bowen-Pope, D.P.  
 J. Biol. Chem. 273, 23929-23937, 1998  
 A>Title: Proliferating and migrating mesangial cells responding to injury express a novel  
 A:Reference number: Z17986; MUID:98395110; PMID:9727007  
 A:Accession: T14328  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2302 <WRI>  
 A:Cross-references: EMBL:AF063249; NID:g3300095; PID:g3300096; PIDN:AAC34801.1  
 A:Experimental source: strain Wistar  
 C:Genetics:  
 A:Note: FTRPQ  
 C:Keywords: phosphoric monoester hydrolase  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-2302/Product: protein-tyrosine phosphatase receptor type, GMCI #status predicted

Query Match 3.5%; Score 14; DB 2; Length 2302;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 2201 VHCAGVGRGTGVPI 2214

R:Gershon, T.R.; Baker, M.; Nitsch, M.; Wu, P.; Macagno, E.R.  
 submitted to the EMBL Data Library, December 1997  
 A>Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed in  
 A:Reference number: Z20939  
 A:Accession: T30938  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2051 <GER>  
 A:Cross-references: EMBL:AF017083; NID:g2695654; PID:g2695655; PIDN:AAB91460.1  
 C:Genetics:  
 A:Gene: LAR2  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 C:Keywords: phosphoric monoester hydrolase  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-2302/Product: protein-tyrosine phosphatase receptor type, GMCI #status predicted

Query Match 3.5%; Score 14; DB 2; Length 2051;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 1981 VHCAGVGRGTGVPI 1994

RESULT 20  
 T15125  
 hypothetical protein T20B6.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T15125  
 R:Beck, C.; Wamsley, P.  
 submitted to the EMBL Data Library, April 1997  
 A>Description: The sequence of C. elegans cosmid T20B6.  
 A:Reference number: Z18297  
 A:Accession: T15125  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-184 <BEC>  
 A:Cross-references: EMBL:AF000193; NID:g1946986; PID:g1946987; PIDN:AAB52889.1; GSPDB C  
 A:Experimental source: strain Bristol N2; clone T20B6  
 C:Genetics:  
 A:Gene: CESP-T20B6.1  
 A:Map position: 3

Query Match 3.5%; Score 14; DB 2; Length 2302;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 2201 VHCAGVGRGTGVPI 2214

RESULT 21  
 T15125  
 hypothetical protein T20B6.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T15125  
 R:Beck, C.; Wamsley, P.  
 submitted to the EMBL Data Library, April 1997  
 A>Description: The sequence of C. elegans cosmid T20B6.  
 A:Reference number: Z18297  
 A:Accession: T15125  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-184 <BEC>  
 A:Cross-references: EMBL:AF000193; NID:g1946986; PID:g1946987; PIDN:AAB52889.1; GSPDB C  
 A:Experimental source: strain Bristol N2; clone T20B6  
 C:Genetics:  
 A:Gene: CESP-T20B6.1  
 A:Map position: 3

Query Match 3.5%; Score 14; DB 2; Length 2302;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 2201 VHCAGVGRGTGVPI 2214

RESULT 22  
 T15125  
 hypothetical protein T20B6.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T15125  
 R:Beck, C.; Wamsley, P.  
 submitted to the EMBL Data Library, April 1997  
 A>Description: The sequence of C. elegans cosmid T20B6.  
 A:Reference number: Z18297  
 A:Accession: T15125  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-184 <BEC>  
 A:Cross-references: EMBL:AF000193; NID:g1946986; PID:g1946987; PIDN:AAB52889.1; GSPDB C  
 A:Experimental source: strain Bristol N2; clone T20B6  
 C:Genetics:  
 A:Gene: CESP-T20B6.1  
 A:Map position: 3

Query Match 3.5%; Score 14; DB 2; Length 2302;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 2201 VHCAGVGRGTGVPI 2214

RESULT 23  
 T15125  
 hypothetical protein T20B6.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T15125  
 R:Beck, C.; Wamsley, P.  
 submitted to the EMBL Data Library, April 1997  
 A>Description: The sequence of C. elegans cosmid T20B6.  
 A:Reference number: Z18297  
 A:Accession: T15125  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-184 <BEC>  
 A:Cross-references: EMBL:AF000193; NID:g1946986; PID:g1946987; PIDN:AAB52889.1; GSPDB C  
 A:Experimental source: strain Bristol N2; clone T20B6  
 C:Genetics:  
 A:Gene: CESP-T20B6.1  
 A:Map position: 3

Query Match 3.5%; Score 14; DB 2; Length 2302;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVPI 370  
 DB 2201 VHCAGVGRGTGVPI 2214

A; Introns: 60/1; 113/2

Query Match 3.0%; Score 12; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 0.00029;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
|||||  
DB 155 LVHCSAGVGRGTG 156

# RESULT 21

JC4155  
N; Alternate names: PE2 protein; protein-tyrosine-phosphatase/ezrin-like protein  
C; Species: Homo sapiens (man)  
C; Date: 27-Aug-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
C; Accession: JC4155  
R; Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.R.  
Biochem. Biophys. Res. Commun. 209, 959-965, 1995  
A; Title: PE2: a novel human cDNA encoding protein tyrosine phosphatase and ezrin-like domain  
A; Reference number: JC4155; MUID: 95251727; PMID: 7733990  
A; Accession: JC4155  
A; Molecule type: mRNA  
A; Residues: 1-1187 <SMI>  
A; Cross-references: EMBL:X82676; NID:G3292753; PIDN:CAA57993.1; PID:G809029  
A; Experimental source: breast  
C; Genetics:  
A; Gene: GDB:PTPN14  
A; Cross-references: GDB:454485  
A; Map position: 1q32.2-1q32.2  
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-binding domain  
C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F; 23-302/Domain: protein 4.1 membrane-binding domain homology <B41>  
F; 566-575/Region: proline-rich  
F; 709-716/Region: acidic  
F; 933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F; 1121/Active site: Cys (phosphocysteine intermediate) #status predicted  
F; 1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 12; DB 1; Length 1187;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 368  
|||||  
DB 1119 VHCAGVGRGTG 1130

# RESULT 22

JC2366  
N; Alternate names: PE2 protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phosphatase  
C; Species: Mus musculus (house mouse)  
C; Date: 24-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
C; Accession: JC2366  
R; Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.  
Biochem. Biophys. Res. Commun. 203, 479-484, 1994  
A; Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskeletal protein  
A; Reference number: JC2366; MUID: 94354845; PMID: 8074693  
A; Accession: JC2366  
A; Molecule type: mRNA  
A; Residues: 1-1189 <SAW>  
A; Cross-references: GDB:D31842; NID:G507330; PIDN:BAA06628.1; PID:G507331  
A; Experimental source: thymus  
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-binding domain  
C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F; 23-402/Domain: protein 4.1 membrane-binding domain homology <B41>  
F; 566-575/Region: proline-rich  
F; 712-718/Region: acidic  
F; 935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F; 1123/Active site: Cys (phosphocysteine intermediate) #status predicted  
F; 1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 12; DB 1; Length 1189;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 368  
|||||  
DB 1121 VHCAGVGRGTG 1132

# RESULT 23

T22672  
N; Hypothetical protein F54F12.1 - Caenorhabditis elegans  
C; Species: Caenorhabditis elegans  
C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C; Accession: T22672  
R; Barlow, K.  
Submitted to the EMBL Data Library, November 1996  
A; Reference number: Z19597  
A; Accession: T22672  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: DNA  
A; Residues: 1-1217 <WIL>  
A; Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:PF5  
A; Experimental source: clone F54F12  
C; Genetics:  
A; Gene: CESP:F54F12.1  
A; Map position: 3  
A; Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

Query Match 3.0%; Score 12; DB 2; Length 1217;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
|||||  
DB 1068 LVHCSAGVGRGTG 1079

# RESULT 24

S68700  
N; HTP beta-like tyrosine phosphatase precursor - mouse  
C; Species: Mus musculus (house mouse)  
C; Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C; Accession: S68700  
R; Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Saitoh, T.; Ohsugi, M.; Yamamoto, T.  
FEBS Lett. 378, 7-14, 1996  
A; Title: Molecular cloning and characterization of Byp, a murine receptor-type tyrosinase  
A; Reference number: S68700; MUID: 96140699; PMID: 8549806  
A; Accession: S68700  
A; Status: preliminary; nucleic acid sequence not shown  
A; Molecule type: mRNA  
A; Residues: 1-1238 <KUR>  
A; Cross-references: GB:D45212; NID:G1208432; PIDN:BAA08146.1; PID:G1208433  
C; Genetics:  
A; Map position: 2E1-2  
C; Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III rep  
C; Keywords: phosphoprotein  
F; 1-28/Domain: signal sequence #status predicted <SIG>  
F; 29-1238/Product: HTP beta-like tyrosine phosphatase #status predicted <MAT>  
F; 267-347/Domain: fibronectin type III repeat homology <3PR>  
F; 966-1188/Domain: protein-tyrosine-phosphatase homology <PTP>  
F; 1140/Active site: Cys (phosphocysteine intermediate) #status predicted  
F; 1146/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 12; DB 2; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
|||||  
DB 1137 LVHCSAGVGRGTG 1148



```

RESULT 25
138670
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human
N:Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 22-Jun-1999
C:Accession: 138670; 152599
R:Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A:Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced
A:Reference number: 138670; MUID:95024024; PMID:17937872
A:Accession: 138670
A:Molecule type: mRNA
A:Residues: 1-1337 <RES>
A:Cross-references: EMBL:U10886; NID:9558754; PID:9558755
A:Experimental source: HeLa cells
R:Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
Blood 84, 4186-4194, 1994
A:Title: Molecular cloning, characterization, and chromosomal localization of a novel pr
A:Reference number: 152599; MUID:95086212; PMID:7994032
A:Accession: 152599
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-216, 'LTVGVKAA', 225-260, 'G', 262-285, 'GTGGGLDASWTSRRA', 302, 'S', 304, 'TAPVHDE
A:Cross-references: GB:D37781; NID:9633072; PIDN:BA07035.1; PID:9633073
C:Comment: Enhanced expression of this protein with increasing cell density suggests a r
C:Genetics:
A:Gene: GDB:PTPRJ
A:Cross-references: GDB:385040; OMIM:600925
A:Map position: 19q13.4-19q13.4
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
A:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repea
A:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
A:1-35/Domain: signal sequence #status predicted <SIG>
A:136-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT>
A:118-197/Domain: fibronectin type III repeat homology <3FNB>
A:208-283/Domain: fibronectin type III repeat homology <3FNB>
A:284-356/Domain: fibronectin type III repeat homology <3FNB> #status atypical <3FNC>
A:365-445/Domain: fibronectin type III repeat homology <3FND>
A:453-530/Domain: fibronectin type III repeat homology <3FNE>
A:539-617/Domain: fibronectin type III repeat homology <3FNE>
A:720-804/Domain: fibronectin type III repeat homology <3FNG>
A:792-988/Domain: transmembrane #status predicted <TMN>
A:1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
A:72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,603,6
A:1239/Active site: Cys (phosphocysteine intermediate) #status predicted
A:1245/Binding site: substrate phosphate (Arg) #status predicted
Query Match 3.0%; Score 12; DB 1; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.0019; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;
C:Genetics:
A:Gene: GDB:PTPRG; D3S1249
A:Cross-references: GDB:127351; OMIM:176886
A:Map position: 3p14.2-3p14.2
A:Superfamily: protein-tyrosine-phosphatase, receptor type gamma precursor - mouse
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C:Accession: B48148
R:Barnea, G.; Silvennoinen, O.; Shaanan, B.; Honegger, A.M.; Canoll, P.D.; D'Eustachio,
Mol. Cell. Biol. 13, 1497-1506, 1993
A:Title: Identification of a carbonic anhydrase-like domain in the extracellular region
A:Reference number: A48148; MUID:93180796; PMID:8382771
A:Accession: B48148
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1442 <BAR>

```

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A:Cross-references: GB:L09562; NID:9293773; PIDN:AAA40022.1; PID:9293774
C:Genetics:
A:Gene: PTPRG
A:Map position: 14
A:Note: extensively polymorphic
A:Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase h
ne-phosphatase homology
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; polymorphism; receptor; tr
F:346-434/Domain: carbonic anhydrase homology <CAH>
F:60-321/Domain: fibronectin type III repeat homology <3FR>
F:742-758/Domain: transmembrane #status predicted <TMN>
F:871-1105/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1172-1396/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1057/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1063/Binding site: substrate phosphate (Arg) #status predicted
Query Match 3.0%; Score 12; DB 1; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 356 LVHCSAGVGRGTG 367
DB 1054 LVHCSAGVGRGTG 1065
RESULT 27
A48148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48148; C36065; S12051
R:Barnea, G.; Silvennoinen, O.; Shaanan, B.; Honegger, A.M.; Canoll, P.D.; D'Eustachio,
Mol. Cell. Biol. 13, 1497-1506, 1993
A:Title: Identification of a carbonic anhydrase-like domain in the extracellular region
A:Reference number: A48148; MUID:93180796; PMID:8382771
A:Accession: A48148
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1445 <BAR>
A:Note: sequence extracted from NCBI backbone (NCBI:125788)
R:Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Hawk, R.; Ravera, M.; Ricca, G.; Jaye,
Proc. Natl. Acad. Sci. U.S.A. 87, 7000-7004, 1990
A:Title: Cloning of three human tyrosine phosphatases reveals a multigene family of re
A:Reference number: A36065; MUID:90384936; PMID:2169617
A:Accession: C36065
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 874-1118; 1175-1409 <KAP>
R:Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine ph
A:Reference number: S12049; MUID:91006018; PMID:2170109
A:Accession: S12051
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 836-1406, 'M', 1408-1445 <KRU>
A:Cross-references: GB:X54132; NID:935793; PIDN:CAA38067.1; PID:935794
C:Genetics:
A:Gene: GDB:PTPRG; D3S1249
A:Cross-references: GDB:127351; OMIM:176886
A:Map position: 3p14.2-3p14.2
A:Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase h
ne-phosphatase homology
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane pr
F:60-321/Domain: carbonic anhydrase homology <CAH>
F:346-434/Domain: fibronectin type III repeat homology <3FR>
F:742-758/Domain: transmembrane #status predicted <TMN>
F:874-1108/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1175-1399/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1060/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1066/Binding site: substrate phosphate (Arg) #status predicted
Query Match 3.0%; Score 12; DB 1; Length 1445;
Best Local Similarity 100.0%; Pred. No. 0.002;

```



Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 |||||  
 DB 1057 LVHCSAGVGRGTG 1068  
 |||||

RESULT 28  
 B36182  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type PTP69D precursor - fruit fly  
 N:Alternate names: protein-tyrosine-phosphatase DPTP  
 C:Species: Drosophila melanogaster  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: B36182  
 R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989  
 A:Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila  
 A:Reference number: A36182; MUID:90046860; PMID:2554325  
 A:Accession: B36182  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1462 <STR>  
 A:Cross-references: GB:M27699; NID:gi58188; PIDN:AAA28842.1; PID:gi58189  
 C:Genetics:  
 A:Gene: PTP69D  
 A:Cross-references: FlyBase:FBgn0014007  
 A:Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D; fibronectin type III  
 phosphatase homology  
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-1462/Product: protein-tyrosine-phosphatase, receptor type PTP69D #status predicted  
 F:29-806/Domain: extracellular #status predicted <EXT>  
 F:38-114/Domain: immunoglobulin homology <IM1>  
 F:147-216/Domain: immunoglobulin homology <IM2>  
 F:807-823/Domain: transmembrane #status predicted <TMN>  
 F:824-1462/Domain: intracellular #status predicted <INT>  
 F:917-1145/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:121-1439/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:45-1154-214/Disulfide bonds: #status predicted  
 F:1097/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1103/Binding site: substrate phosphate (Arg) #status predicted  
 F:1191/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1197/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 12; DB 1; Length 1462;  
 Best Local Similarity 100.0%; Pred. No. 0.002;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 |||||  
 DB 1094 LVHCSAGVGRGTG 1105  
 |||||

RESULT 29  
 A55148  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat  
 N:Alternate names: OST-PTP; osteoclastic protein-tyrosine-phosphatase  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A55148  
 R:Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.  
 J. Biol. Chem. 269, 30659-30667, 1994  
 A:Title: Identification of a hormonally regulated protein tyrosine phosphatase associated with osteoclasts  
 A:Reference number: A55148; MUID:95074080; PMID:7527035  
 A:Accession: A55148  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1711 <NAU>  
 A:Cross-references: GB:B36884  
 C:Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosine  
 phosphatase domains.  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III repeat  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane protein

F:19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted  
 F:1174-1398/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:1350/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 3.0%; Score 12; DB 1; Length 1711;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 |||||  
 DB 1347 LVHCSAGVGRGTG 1358  
 |||||

RESULT 30  
 T27722  
 hypothetical protein ZK1251.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1998 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T27722  
 R:McMurray, A.  
 submitted to the EMBL Data Library, December 1995  
 A:Reference number: Z20411  
 A:Accession: T27722  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-198 <WTL>  
 A:Cross-references: EMBL:Z68222; PIDN:CAA92501.1; GSPDB:GN00022; CESP:ZK1251.5  
 A:Experimental source: clone ZK1251  
 C:Genetics:  
 A:Gene: CESP:ZK1251.5  
 A:Map position: 4  
 A:Introns: 46/3; 101/2; 185/3

Query Match 2.7%; Score 11; DB 2; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 0.0033;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASAGVGRGTG 367  
 |||||  
 DB 106 VHCASAGVGRGTG 116  
 |||||

RESULT 31  
 A40169  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type zeta - rat (fragment)  
 N:Alternate names: protein-tyrosine-phosphatase beta; protein-tyrosine-phosphatase PTP  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 05-Jun-1992 #sequence\_revision 05-Jun-1992 #text\_change 24-Apr-1998  
 C:Accession: A40169  
 R:Guan, K.; Dixon, J.E.  
 Science 249, 553-556, 1990  
 A:Title: Protein tyrosine phosphatase activity of an essential virulence determinant in  
 A:Reference number: A40169; MUID:90341778; PMID:2166336  
 A:Accession: A40169  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-256 <GUA>  
 C:Function:  
 A:Description: may be involved in the regulation of specific developmental processes in  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type zeta; carbonic anhydrase ho  
 C:Keywords: brain; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; recep  
 F:6-237/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:189/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:195/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 0.0042;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASAGVGRGTG 367  
 |||||  
 DB 187 VHCASAGVGRGTG 197  
 |||||

## RESULT 32

39862  
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: protein D0815; protein YD230w  
 C:Species: Saccharomyces cerevisiae  
 C:Accession: A39862; S67793  
 C:Date: 30-Dec-1991 #sequence\_revision 08-Mar-1996 #text\_change 21-Jul-2000  
 C:Biochem. J. 266, 12964-12970, 1991  
 C:Title: Cloning and expression of a yeast protein tyrosine phosphatase.  
 C:Reference number: A39862; MUID:91302312; PMID:1649172  
 C:Accession: A39862  
 C:Genetics:  
 A:Molecule type: DNA  
 A:Residues: 1-335 <GUA>  
 A:Cross-references: GB:M64062; NID:g172295; PIDN:AAA34923.1; PID:g172296  
 C:Rasmussen, S.W.  
 A:Reference number: S67778  
 A:Accession: S67793  
 A:Molecule type: DNA  
 A:Residues: 1-335 <RAS>  
 A:Cross-references: EMBL:Z74278; NID:g1431387; PIDN:CAA98809.1; PID:g1431388; GSPDB:GN000000000  
 A:Experimental source: strain S288C  
 C:Genetics:  
 A:Gene: SGP:PTP1; MIPS:YD230w  
 A:Cross-references: SGD:S0002389; MIPS:YD230w  
 A:Map position: 4L  
 C:Superfamily: Saccharomyces protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase, phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:1-303/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:52-303/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:252/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:258/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 0.0054;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367

Db 250 VHCAGVGRTG 260

## RESULT 33

158540  
 protein-tyrosine-phosphatase (EC 3.1.3.48) ctp1 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 23-Jul-1999  
 C:Accession: I56540  
 C:Biochem. J. 266, 12964-12970, 1991  
 C:Title: Protein tyrosine phosphatases expressed in the developing rat brain.  
 C:Reference number: I56540; MUID:94045925; PMID:8229209  
 C:Accession: I56540  
 C:Genetics:  
 A:Molecule type: mRNA  
 A:Residues: 1-398 <RES>  
 A:Cross-references: EMBL:U03273; NID:9414996; PIDN:AA52124.1; PID:g414997  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <PTP>  
 F:225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <PTP>  
 F:109/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 0.0064;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367

Db 107 VHCAGVGRTG 117

## RESULT 34

149372  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O - mouse (fragment)  
 N:Alternate names: GLPPI; glomerular epithelial protein 1  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 21-Feb-1997 #text\_change 23-Jul-1999  
 C:Accession: I49372; I49373; I49374  
 C:Biochem. J. 266, 12964-12970, 1991  
 C:Title: A heteromeric protein tyrosine phosphatase, PTPphi, is regulated by CSP-1 in  
 A:Reference number: I49372; MUID:96070847; PMID:752997  
 A:Accession: I49372  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-405 <RES>  
 A:Cross-references: EMBL:U37465; NID:g1063639; PIDN:AA52311.1; PID:g1063640  
 A:Accession: I49373  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-65,94-405 <RES>  
 A:Cross-references: EMBL:U37466; NID:g1063641; PIDN:AA52312.1; PID:g1063642  
 A:Accession: I49374  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 119-405 <RES>  
 A:Cross-references: EMBL:U37467; NID:g1063643; PIDN:AA52313.1; PID:g1063644  
 C:Comment: Expression of the various forms is tissue specific. GLPPI is expressed in k  
 Cytosolic form is expressed at very low levels in macrophages.  
 C:Genetics:  
 A:Gene: PTPphi  
 A:Map position: 6q  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repe  
 C:Keywords: alternative initiators; alternative splicing; brain; cardiac muscle; glyco  
 ne-specific phosphatase  
 F:1-405/Product: protein tyrosine phosphatase phi, long form #status predicted <PHIL>  
 F:1-65,94-405/Product: protein tyrosine phosphatase phi, short form #status predicted <PHIL>  
 F:9-33/Domain: transmembrane #status predicted <TMN>  
 F:34-405/Domain: intracellular #status predicted <INT>  
 F:119-405/Product: protein tyrosine phosphatase phi, cytosolic form #status predicted <  
 F:151-373/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:325/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:331/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 0.0065;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 VYATQGLPPT 241

Db 196 VYATQGLPPT 206

## RESULT 35

S68250  
 protein-tyrosine-phosphatase (EC 3.1.3.48) - rabbit  
 N:Alternate names: phosphotyrosyl phosphatase  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 05-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
 C:Accession: S68250  
 C:Biochem. J. 316, 515-523, 1996  
 C:Title: Molecular cloning and expression of a unique rabbit osteoclastic phosphotyrosy  
 A:Reference number: S68250; MUID:96257745; PMID:8687395  
 A:Accession: S68250  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-405 <WUL>

Query Match 2.7%; Score 11; DB 2; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 0.0064;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Cross-references: EMBL:U32587; NID:gl104388; PIDN:AAB16824.1; PID:gl104389  
 C;Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat  
 C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F;151-373/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F;325/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F;331/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 0.0065;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPET 241  
 |||||  
 DB 196 YIATQGLPET 206

RESULT 36  
 T25992  
 hypothetical protein ZK354.8 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T25992  
 R;Johnson, D.; Wamley, P.; Bradshaw, H.  
 submitted to the EMBL Data Library, February 1997  
 A;Description: The sequence of C. elegans cosmid ZK354.  
 A;Reference number: Z20120  
 A;Accession: T25992  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-483 <JOH>  
 A;Cross-references: EMBL:U08172; PIDN:AAB42260.1; GSPDB:GN00022; CESP:ZK354.8  
 A;Experimental source: strain Bristol N2; clone ZK354  
 C;Genetics:  
 A;Gene: CESP:ZK354.8  
 A;Map position: 4  
 A;Introns: 7/1; 70/3; 180/2; 256/2; 331/3; 386/2; 470/3

Query Match 2.7%; Score 11; DB 2; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 0.0077;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
 |||||  
 DB 391 VHCAGVGRGTG 401

RESULT 37  
 A44267  
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - slime mold (Dictyostelium)  
 C;Species: Dictyostelium discoideum  
 C;Date: 30-Apr-1993 #sequence\_revision 08-Mar-1996 #text\_change 24-Apr-1998  
 C;Accession: A44267  
 R;Howard, P.X.; Sefton, B.M.; Firtel, R.A.  
 Cell 71, 637-647, 1992  
 A;Title: Analysis of a spatially regulated phosphotyrosine phosphatase identifies tyrosi  
 A;Reference number: A44267; MUID:93045662; PMID:1423620  
 A;Accession: A44267  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA; DNA  
 A;Residues: 1-521 <HOW>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:117713)  
 C;Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 1; protein-  
 C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F;121-459/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>  
 F;310/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F;316/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 0.0063;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
 |||||

Db 308 VHCAGVGRGTG 318

## RESULT 38

A40449

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type pyp1 - fission yeast (Sch  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Dec-1999  
 C;Accession: A40449; T38410  
 R;Ottillie, S.; Chernoff, J.; Hannig, G.; Hoffman, C.S.; Erikson, R.L.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 3455-3459, 1991  
 A;Title: A fission-yeast gene encoding a protein with features of protein-tyrosine-pho  
 A;Reference number: A40449; MUID:91195370; PMID:1849659  
 A;Accession: A40449  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-550 <OTT>  
 A;Cross-references: GB:M63257; NID:gl173441; PIDN:AAB35328.1; PID:gl173442  
 R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL Data Library, April 1996  
 A;Reference number: Z21792  
 A;Accession: T38410  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-550 <BRO>  
 A;Cross-references: EMBL:Z73100; PIDN:CAA97367.1; GSPDB:GN00066; SPDB:SPAC26F1.10C  
 A;Experimental source: strain 972H-; cosmid c26F1  
 C;Genetics:  
 A;Gene: SPAC26F1.10C  
 A;Map position: 1  
 C;Superfamily: Schizosaccharomyces protein-tyrosine-phosphatase, nonreceptor type pyp1  
 C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat  
 F;295-528/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F;470/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F;476/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 550;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367

|||||

DB 468 VHCAGVGRGTG 478

## RESULT 39

S17671

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 22-Nov-1993 #sequence\_revision 15-Mar-1996 #text\_change 23-Jul-1999  
 C;Accession: S17671; S40287  
 R;Gebbinck, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L  
 FEBS Lett. 290, 123-130, 1991  
 A;Title: Cloning, expression and chromosomal localization of a new putative receptor-1;  
 A;Reference number: S17669; MUID:92008644; PMID:1655529  
 A;Accession: S17671  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-583 <GB>  
 A;Cross-references: EMBL:X58289  
 R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A;Description: Assessment of the expression levels of murine protein-tyrosine phosphat  
 A;Reference number: S40280  
 A;Accession: S40287  
 A;Molecule type: mRNA  
 A;Residues: 377-483 'T', 485-486 <HEN>  
 A;Cross-references: EMBL:Z23056; NID:9438149; PIDN:CAA80591.1; PID:9438150  
 C;Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III  
 C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane pr  
 F;311-536/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F;488/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F;494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 583;  
 Best Local Similarity 100.0%; Pred. No. 0.0092;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
 |||||  
 DB 486 VHCSAGVGRGTG 496

RESULT 40  
 JC6132  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - mouse  
 N:Alternate names: phosphotyrosine phosphatase; protein-tyrosine-phosphate phosphohydrolase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 21-Jun-2002  
 C:Accession: JC6132  
 R:Schmidt, A.; Rutledge, S.J.; Endo, N.; Onas, E.E.; Tanaka, H.; Wesolowski, G.; Liu, C.  
 Proc. Natl. Acad. Sci. U.S.A. 93, 3068-3073, 1996  
 A:Title: Protein-tyrosine phosphatase activity regulates osteoclast formation and function  
 A:Reference number: JC6132; MUID:96181534; PMID:8610169  
 A:Contents: Bone marrow cell  
 A:Accession: JC6132  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-699 <SCH>  
 A:Cross-references: GB:U40280; NID:gl373052; PIDN:AAB02190.1; PID:gl373053  
 C:Comment: This enzyme plays an important role in osteoclast formation and function in bone  
 C:Genetics:  
 A:Gene: ptp  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyrosine  
 F:77-697/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:158-382/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:334/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:340/Binding site: substrate phosphate (Arg) #status predicted  
 F:629/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:635/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 699;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
 |||||  
 DB 332 VHCSAGVGRGTG 342

RESULT 41  
 S12053  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S12053  
 R:Krueger, N.X.; Streuli, M.; Saito, H.  
 EMBO J. 9, 3241-3252, 1990  
 A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases  
 A:Reference number: S12049; MUID:91006018; PMID:2170109  
 A:Accession: S12053  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-700 <KRU>  
 A:Cross-references: GB:X54134; NID:g35791; PIDN:CAA38069.1; PID:g35792  
 C:Genetics:  
 A:Gene: GDB:PTPRE  
 A:Cross-references: GDB:131385; OMIM:600926  
 A:Map position: 10q26-10q26  
 C:Function:  
 A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-700/Product: protein-tyrosine-phosphatase, receptor type epsilon #status predicted  
 F:47-63/Domain: transmembrane #status predicted <TM>  
 F:78-698/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:159-383/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:335/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:341/Binding site: substrate phosphate (Arg) #status predicted  
 F:630/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:636/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 700;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
 |||||  
 DB 333 VHCSAGVGRGTG 343

## RESULT 42

S28391  
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type pyp2 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Dec-1999  
 C:Accession: S28391; A45030; T37961  
 R:Millar, J.B.A.; Russell, P.; Dixon, J.E.; Guan, K.L.  
 EMBO J. 11, 4943-4952, 1992  
 A:Title: Negative regulation of mitosis by two functionally overlapping PTPases in fission yeast  
 A:Reference number: S28391; MUID:93099869; PMID:1464319  
 A:Accession: S28391  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA

A:Residues: 1-711 <MTL>  
 A:Cross-references: GB:S51320; NID:g261946; PIDN:AAB24544.1; PID:g261947  
 R:Ottile, S.; Chernoff, J.; Hannig, G.; Hoffman, C.S.; Erikson, R.L.  
 Mol. Cell. Biol. 12, 5571-5580, 1992  
 A:Title: The fission yeast genes pyp1+ and pyp2+ encode protein tyrosine phosphatases  
 A:Reference number: A45030; MUID:93078758; PMID:1448087  
 A:Accession: A45030  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-711 <OPT>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:113076)  
 R:Devlin, K.; Church, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
 Submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z21757  
 A:Accession: T37961  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-711 <DEV>  
 A:Cross-references: EMBL:Z99531; PIDN:CAB16711.1; GSPDB:GN000066; SPDB:SPAC19D5.01  
 A:Experimental source: strain 972h-; cosmid c19D5  
 C:Genetics:  
 A:Gene: pyp2  
 A:Map position: 1

C:Superfamily: Schizosaccharomyces protein-tyrosine-phosphatase, nonreceptor type pyp2,  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:458-687/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:630/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:636/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
 |||||  
 DB 628 VHCSAGVGRGTG 638

## RESULT 43

JCL285  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - rat  
 N:Alternate names: protein-tyrosine-phosphatase LRP

C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: J01285; J23253; J0450  
 R:Moriyama, T.; Fujiwara, Y.; Imai, E.; Takenaka, M.; Kawanishi, S.; Inoue, T.; Noguchi, R.  
 Biochem. Biophys. Res. Commun. 188, 34-39, 1992  
 A>Title: cDNA cloning of rat LRP, a receptor like protein tyrosine phosphatase, and evidence submitted to the EMBL Data Library, June 1990  
 A:Reference number: J01285; MUID:93038682; PMID:1417854  
 A:Accession: J01285  
 A:Molecule type: mRNA  
 A:Residues: 1-796 <MOR>  
 A:Experimental source: Kidney  
 A>Note: The authors translated the codon TCC for residue 788 as Ala  
 R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
 Biochem. J. 284, 569-576, 1992  
 A>Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three A:Reference number: J23126; MUID:92287069; PMID:1599438  
 A:Accession: J23126  
 A:Molecule type: mRNA  
 A:Residues: 254-267, 'I', 269-354, 'T', 356-501 <HAS>  
 R:Zhang, W.R.; Goldstein, B.J.  
 Biochem. Biophys. Res. Commun. 178, 1291-1297, 1991  
 A>Title: Identification of skeletal muscle protein-tyrosine phosphatases by amplification A:Reference number: J0450; MUID:91337074; PMID:1651716  
 A:Accession: J0450  
 A:Molecule type: mRNA  
 A:Residues: 324-354, 'T', 356-434 <ZHA>  
 A:Experimental source: skeletal muscle, strain Sprague-Dawley  
 C:Function:  
 A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate A>Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor A:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane protein F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-796/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted <M F:20-148/Domain: extracellular #status predicted <EXT>  
 F:149-165/Domain: transmembrane #status predicted <INT>  
 F:166-796/Domain: intracellular #status predicted <INT>  
 F:178-794/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:253-484/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:552-774/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:436/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:442/Binding site: substrate phosphate (Arg) #status predicted  
 F:726/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:732/Binding site: substrate phosphate (Arg) #status predicted  
 Query Match 2.7%; Score 11; DB 1; Length 796;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRG 367  
 DB 434 VHCAGVGRG 444  
 RESULT 44  
 A36065  
 C:Species: Homo sapiens (man)  
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A36065; J12049; J17371; J12905; J13085  
 R:Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Hawk, R.; Raver, M.; Ricca, G.; Jaye, Proc. Natl. Acad. Sci. U.S.A. 87, 7000-7004, 1990  
 A>Title: Cloning of three human tyrosine phosphatases reveals a multigene family of receptors A:Reference number: A36065; MUID:90384936; PMID:2169617  
 A:Accession: A36065  
 A:Molecule type: mRNA  
 A:Status: preliminary; not compared with conceptual translation  
 A:Residues: 1-802 <KAP>  
 A:Cross-references: GB:M34668; NID:G190738; PIDN:AAA36528.1; PID:G130739  
 R:Kueger, N.X.; Struelli, M.; Saito, H.  
 EMBO J. 9, 3241-3252, 1990  
 A>Title: Structural diversity and evolution of human receptor-like protein tyrosine phosph

A:Reference number: S12049; MUID:91006018; PMID:2170109  
 A:Accession: S12049  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-138, 148-802 <KRU>  
 A:Cross-references: GB:X54130; NID:935785; PIDN:CAA38065.1; PID:935786  
 R:Jirik, F.R.; Janzen, N.M.; Melhado, I.G.; Harder, K.W.; Leslie, K.B.  
 submitted to the EMBL Data Library, June 1990  
 A:Description: Isolation of a cDNA encoding a novel protein-tyrosine phosphatase from A:Reference number: S17371  
 A:Accession: S17371  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-121, 'P', 123-138, 148-199, 'G', 201-203, 'C', 205-802 <JIR>  
 A:Cross-references: EMBL:X53364  
 R:Jirik, F.R.; Janzen, N.M.; Melhado, I.G.; Harder, K.W.  
 FEBS Lett. 273, 239-242, 1990  
 A>Title: Cloning and chromosomal assignment of a widely expressed human receptor-like A:Reference number: S12905; MUID:91032191; PMID:2172030  
 A:Accession: S12905  
 A:Molecule type: mRNA  
 A:Residues: 1-61, 'V', 62-82, 84-121, 'P', 123-138, 148-199, 'G', 201-203, 'C', 205-802 <J12>  
 R:Ohagi, S.; Nishi, M.; Steiner, D.F.  
 Nucleic Acids Res. 18, 7159, 1990  
 A>Title: Sequence of a cDNA encoding human LRP (leukocyte common antigen-related pepti A:Reference number: S13085; MUID:91088320; PMID:2175890  
 A:Accession: S13085  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-113, 'M', 115-138, 148-288, 'E', 290-366, 'A', 368-492, 'S', 494-785, 'E', 787-802 A:Cross-references: EMBL:X54890; NID:932312; PIDN:CAA38662.1; PID:932313  
 C:Genetics:  
 A:Gene: GDB:PTPRA; PTPA  
 A:Cross-references: GDB:126732; OMIM:176884  
 A:Map position: 20p13-20p13  
 C:Function:  
 A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate A>Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-802/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted  
 F:20-154/Domain: extracellular #status predicted <EXT>  
 F:155-171/Domain: transmembrane #status predicted <INT>  
 F:172-802/Domain: intracellular #status predicted <INT>  
 F:184-800/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
 F:265-490/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F:558-780/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F:442/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:448/Binding site: substrate phosphate (Arg) #status predicted  
 F:732/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:738/Binding site: substrate phosphate (Arg) #status predicted  
 Query Match 2.7%; Score 11; DB 1; Length 802;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRG 367  
 DB 440 VHCAGVGRG 450  
 RESULT 45  
 A47373  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 21-Jan-2000  
 C:Accession: A47373; B35501; A35501; P80367; S40285; S40286; A36004; D61180  
 R:Wong, E.C.; Muller, J.E.; Thomas, M.L.  
 Genomics 17, 33-36, 1993  
 A>Title: Leukocyte common antigen-related phosphatase (LRP) gene structure: conservati

A:Reference number: A47373; MUID:94010906; PMID:8406469  
A:Accession: A47373  
A:Molecule type: DNA  
A:Residues: 1-829 <WON>  
A:Cross-references: GB:113607  
A:Note: sequence extracted from NCBI backbone (NCBIN:137623, NCBIP:137624)  
R:Matthews, R.J.; Cabir, E.D.; Thomas, M.L.  
Proc. Natl. Acad. Sci. U.S.A. 87, 4444-4448, 1990  
A:Title: Identification of an additional member of the protein-tyrosine-phosphatase family  
A:Reference number: A35501; MUID:90280391; PMID:2162042  
A:Accession: B35501  
A:Molecule type: mRNA  
A:Residues: 1-829 <MA1>  
A:Cross-references: GB:M36033; NID:G198876; PIDN:AAA9448.1; PID:G198877; GB:M33671  
A:Note: the authors translated the codon GAT for residue 30 as Tyr  
A:Accession: A35501  
A:Molecule type: mRNA  
A:Residues: 1-267, 'Y', 305-829 <MA2>  
A:Cross-references: GB:M36033; GB:M33671  
R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Knuijer, W.  
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992  
A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase  
A:Reference number: JH0609; MUID:92272714; PMID:1590786  
A:Accession: P80367  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 322-325, 'G', 327-356 <DEN>  
A:Experimental source: embryonal carcinoma cell, P19 cell  
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
submitted to the EMBL Data Library, June 1993  
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatases  
A:Reference number: S40280  
A:Accession: S40285  
A:Molecule type: mRNA  
A:Residues: 358-467 <HEN>  
A:Cross-references: EMBL:Z23054; NID:G438145; PIDN:CAA80589.1; PID:G438146  
A:Accession: S40286  
A:Molecule type: mRNA  
A:Residues: 651-756 <HE2>  
A:Cross-references: EMBL:Z23055; NID:G438147; PIDN:CAA80590.1; PID:G438148  
R:Sap, J.; D'Eustachio, P.; Givol, D.; Schlessinger, J.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6112-6116, 1990  
A:Title: Cloning and expression of a widely expressed receptor tyrosine phosphatase.  
A:Reference number: A36004; MUID:90349565; PMID:2166945  
A:Accession: A36004  
A:Molecule type: mRNA  
A:Residues: 1-230, 'L', 232-267, 'Y', 305-410, 'S', 412-829 <SAP>  
A:Cross-references: GB:M34668  
R:Yi, T.; Cleveland, J.L.; Ihle, J.N.  
Blood 78, 2222-2228, 1991  
A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by  
A:Reference number: A61180; MUID:92032882; PMID:1932742  
A:Accession: D61180  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 358-467 <YIA>  
C:Genetics:  
A:Map position: 2  
C:Function:  
A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate  
A:Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor  
C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-142/Domain: protein-tyrosine-phosphatase, receptor type alpha #status predicted <M  
F:167-829/Domain: intracellular #status predicted <EXT>  
F:143-156/Domain: transmembrane #status predicted <TM>  
F:175-827/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:585-807/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:21, 47, 51, 68, 86, 104, 124/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:469/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:475/Binding site: substrate phosphate (Arg) #status predicted

F:759/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:765/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 829;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367  
DB 467 VHCAGVGRTG 477

## RESULT 45

A:Accession: A49724  
A:Title: protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human  
N:Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SAP  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence\_revision 23-Feb-1996 #text\_change 16-Jun-2000  
C:Accession: A49724  
R:Matosaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, J.  
J. Biol. Chem. 269, 2075-2081, 1994  
A:Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase  
A:Reference number: A49724; MUID:94124561; PMID:8294459  
A:Accession: A49724  
A:Molecule type: mRNA  
A:Residues: 1-1118 <MATO>  
A:Cross-references: GB:D15049; NID:G475003; PIDN:BAA03645.1; PID:G475004  
C:Genetics:  
A:Gene: GDB:PTPRH; SAP-1  
A:Map position: 19q13.4-19q13.4  
A:Note: highly expressed in colon and pancreatic cancer cells but not in the normal ce.  
C:Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III rep  
C:Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric mono  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:27-110/Domain: fibronectin type III repeat homology <3FNA>  
F:28-761/Domain: extracellular #status predicted <EXT>  
F:116-199/Domain: fibronectin type III repeat homology <3FNB>  
F:205-289/Domain: fibronectin type III repeat homology <3FNC>  
F:296-379/Domain: fibronectin type III repeat homology <3FND>  
F:385-468/Domain: fibronectin type III repeat homology <3FNE>  
F:474-558/Domain: fibronectin type III repeat homology <3FNF>  
F:564-658/Domain: fibronectin type III repeat homology <3FNG>  
F:667-737/Domain: fibronectin type III repeat homology <3FNH>  
F:762-778/Domain: transmembrane #status predicted <TM>  
F:779-1118/Domain: intracellular #status predicted <INT>  
F:846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:35, 78, 83, 107, 132, 149, 172, 196, 203, 286, 304, 312, 329, 352, 376, 383, 401, 436, 439, 470, 490, 558.  
F:1022/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 1118;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367  
DB 1020 VHCAGVGRTG 1030

## RESULT 47

A:Accession: A53661  
A:Title: protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - rabbit  
N:Alternate names: GLEP1; glomerular epithelial protein-1  
N:Contains: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphat  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 07-Oct-1994 #sequence\_revision 08-Feb-1996 #text\_change 22-Jun-1999  
C:Accession: A53661  
R:Thomas, P.E.; Wharram, B.I.; Goyal, M.; Wiggins, J.E.; Holzman, L.B.; Wiggins, R.C.  
J. Biol. Chem. 269, 19953-19962, 1994  
A:Title: GLEP1, a renal glomerular epithelial cell (podocyte) membrane protein-tyrosin  
A:Reference number: A53661; MUID:94327545; PMID:7519601

F:934-1156/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:75-154,189,201,227,278,323,324,370,461,490,700,712,733,790/Binding site: carboxy  
F:1108/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1114/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 1188;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPPT 241  
DB 979 YIATQGLPPT 989  
|||||  
|||||

RESULT 49  
T43148  
probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark  
N;Alternate names: CD45 homology  
C;Species: Heterodontus francisci (horn shark)  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C;Accession: T43148  
R;Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.  
submitted to the EMBL Data Library, August 1995  
A;Reference number: Z22317  
A;Accession: T43148  
A;Status: Preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1200 <OKU>  
C;Cross-references: EMBL:U34750; NID:g1304393; PID:g1335805; PIDN:AAB01087.1  
C;Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain hom  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat

Query Match 2.7%; Score 11; DB 2; Length 1200;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASGVGRTG 367  
DB 749 VHCASGVGRTG 759  
|||||  
|||||

RESULT 50  
S60613  
protein-tyrosine-phosphatase (EC 3.1.3.48) U2 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C;Accession: S60613  
R;Seimiya, H.; Sawabe, T.; Inazawa, J.; Tsuruo, T.  
Oncogene 10, 1731-1738, 1995  
A;Title: Cloning, expression and chromosomal localization of a novel gene for protein  
A;Reference number: S60613; MUID:95273089; PMID:7753550  
A;Accession: S60613  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1216 <SEI>  
C;Cross-references: EMBL:Z48541; NID:g963058; PIDN:CAA8425.1; PID:g963059  
C;Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III rep  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat  
P:529-626/Domain: fibronectin type III repeat homology <PPI>  
P:962-1184/Domain: protein-tyrosine-phosphatase homology <PTP1>  
P:1136/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1142/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 1216;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPPT 241  
DB 1007 YIATQGLPPT 1017  
|||||  
|||||

RESULT 51

A;Accession: A53661  
A;Molecule type: mRNA  
A;Residues: 1-1187 <THO>  
A;Cross-references: GB:U09490; NID:g529411; PID:AAAG1709.1; PID:g529412  
A;Note: authors translated the codon GGC for residue 1101 as Gln  
C;Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repea  
C;Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; recept  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-818/Domain: extracellular #status predicted <EXT>  
F:30-115/Domain: fibronectin type III repeat homology #status atypical <FN3A>  
F:316-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>  
F:328-415/Domain: fibronectin type III repeat homology <FN3D>  
F:431-519/Domain: fibronectin type III repeat homology <FN3E>  
F:528-625/Domain: fibronectin type III repeat homology <FN3F>  
F:630-713/Domain: fibronectin type III repeat homology <FN3G>  
F:721-810/Domain: fibronectin type III repeat homology <FN3H>  
F:811-1187/Domain: protein tyrosine phosphatase phi, long form #status predicted <PHIL>  
F:811-875, 876-1187/Domain: product: protein tyrosine phosphatase phi, short form #status predic  
F:819-843/Domain: transmembrane #status predicted <TM>  
F:844-1187/Domain: intracellular #status predicted <INT>  
F:901-1187/Domain: protein tyrosine phosphatase phi, cytosolic form #status predicted <PHIL>  
F:933-1185/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:75-154,189,201,227,278,323,369,489,699,711,732,789/Binding site: carboxydrate  
F:1107/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1113/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 1187;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPPT 241  
DB 978 YIATQGLPPT 988  
|||||  
|||||

RESULT 48  
A57064  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - human  
N;Alternate names: GLEPPI; glomerular epithelial protein 1  
N;Contains: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphata  
C;Species: Homo sapiens (man)  
C;Date: 03-Oct-1995 #sequence\_revision 08-Feb-1996 #text\_change 22-Jun-1999  
C;Accession: A57064  
R;Wiggins, R.C.; Wiggins, J.E.; Goyal, M.; Wharram, B.L.; Thomas, P.E.  
Genomics 27, 174-181, 1995  
A;Title: Molecular cloning of cDNAs encoding human GLEPPI, a membrane protein tyrosine p  
ne to human chromosome 12p12-p13.  
A;Reference number: A57064; MUID:95394455; PMID:7665166  
A;Accession: A57064  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1188 <HTG>  
A;Cross-references: GB:U20489; NID:g885925; PIDN:AAAG2892.1; PID:g885926  
C;Genetics:  
A;Gene: GDB:PTPRO  
A;Cross-references: GDB:454477; OMIM:600579  
A;Map position: 12p13.3-12p13.1  
C;Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repea  
C;Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; recept  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-819/Domain: extracellular #status predicted <EXT>  
F:30-109/Domain: fibronectin type III repeat homology #status atypical <FN3A>  
F:316-202/Domain: fibronectin type III repeat homology #status atypical <FN3B>  
F:329-409/Domain: fibronectin type III repeat homology <FN3C>  
F:432-520/Domain: fibronectin type III repeat homology <FN3D>  
F:529-619/Domain: fibronectin type III repeat homology <FN3E>  
F:631-714/Domain: fibronectin type III repeat homology <FN3F>  
F:722-804/Domain: fibronectin type III repeat homology <FN3G>  
F:812-1188/Domain: fibronectin type III repeat homology <FN3H>  
F:812-876, 877-1188/Domain: product: protein tyrosine phosphatase phi, long form #status predicted <PHIL>  
F:812-876, 877-1188/Domain: product: protein tyrosine phosphatase phi, short form #status predic  
F:820-844/Domain: transmembrane #status predicted <TM>  
F:845-1188/Domain: intracellular #status predicted <INT>  
F:902-1188/Domain: protein tyrosine phosphatase phi, cytosolic form #status predicted <PHIL>



JC7503

protein-tyrosine-phosphatase (EC 3.1.3.48), a receptor-type - mouse  
 N:Alternate names: phosphotyrosine phosphatase, a receptor-type  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 24-Aug-2001  
 C:Accession: JC7503  
 R:Tomemori, T.; Seki, N.; Suzuki, Y.; Shimizu, T.; Nagata, H.; Konno, A.; Shirasawa, T.  
 Biochem. Biophys. Res. Commun. 276, 974-981, 2000  
 A:Title: Isolation and characterization of murine orthologue of PTP-BK.  
 A:Reference number: JC7503

A:Contents: Brain  
 A:Accession: JC7503  
 A:Molecule type: mRNA  
 A:Residues: 1-1226 <TOM>  
 A:Cross-references: GB:AF295638  
 C:Comment: This enzyme, specifically expressed in brains and kidneys, functions in phosphatase  
 C:Genetics:  
 A:Gene: ptp-bk  
 A:Map position: 6

C:Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat  
 C:Keywords: brain; glycolysis; kidney; phosphoric monoester hydrolase

Query Match 2.7%; Score 11; DB 2; Length 1226;  
 Best Local Similarity 100.0%; Pred. NO. 0.019;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 YIATQGLPET 241

Db 1017 YIATQGLPET 1027

RESULT 52

A54080

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken  
 C:Species: Gallus gallus (chicken)

C>Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 21-Jan-2000

C:Accession: A54080; I50592

R:Yang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.

J. Biol. Chem. 269, 14056-14063, 1994

A:Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in  
 A:Reference number: A54080; MUID:94245724; PMID:8188686

A:Accession: A54080

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1237 <FAN>

A:Cross-references: EMBL:Z21960; NID:9510510; PIDN:CAA79972.1; PID:G510511; GB:L13285  
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:610-834/Domain: protein-tyrosine-phosphatase homology <PTP>

F:796/Active site: Cys (phosphocysteine intermediate) #status predicted

F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 2; Length 1237;

Best Local Similarity 100.0%; Pred. NO. 0.019;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTG 367

Db 784 VHCAGVGRGTG 794

RESULT 53

B48758

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form PS precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: B48758

R:Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.

J. Biol. Chem. 268, 19284-19291, 1993

A:Title: Cloning and expression of two structurally distinct receptor-linked protein-tyr  
 A:Reference number: A48758; MUID:93374907; PMID:8396131

A:Accession: B48758

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1262 &lt;PAN&gt;

A:Cross-references: GB:IL19181

A>Note: the authors translated the codon TGC for residue 27 as Gly, GAG for residue 79  
 727 as Phe, residues 1237-1244 are shown after residue 1262, and, consequently, residu  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology.

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tran  
 F:149-209/Domain: immunoglobulin homology <IMM1>

F:246-300/Domain: immunoglobulin homology <IMM2>

F:318-398/Domain: fibronectin type III repeat homology <FN3A>

F:411-497/Domain: fibronectin type III repeat homology <FN3B>

F:509-590/Domain: fibronectin type III repeat homology <FN3C>

F:600-677/Domain: fibronectin type III repeat homology <FN3D>

F:890-1262/Domain: leukocyte common antigen cytosolic domain homology #status atypical  
 F:967-1188/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1146/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 1262;

Best Local Similarity 100.0%; Pred. NO. 0.019;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 YIATQGLPET 241

Db 1012 YIATQGLPET 1022

RESULT 54

TDRTLT

leukocyte common antigen precursor, splice form 4 - rat

N:Alternate names: CD45; L-CA; Ly-5; T200

N:Contents: leukocyte common antigen precursor, splice form 1; leukocyte common antigen  
 1.3.48)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 04-Dec-1986 #sequence\_revision 05-May-2000 #text\_change 21-Jun-2002

C:Accession: A29450; B29450; C29450; D29450; A0241; A02247; I54569; A45854

R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

EMBO J. 6, 1259-1264, 1987

A:Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) ;  
 A:Reference number: A91067; MUID:87275817; PMID:2440674

A:Accession: A29450

A:Molecule type: mRNA

A:Residues: 20-30,163-218 <BAR1>

A:Cross-references: GB:M25820; GB:M24611; NID:g205153; GB:Y00065; GB:K03039; GB:M10072.

A:Experimental source: splice form 1

A>Note: the translation in GenBank entry RATLCAI, PIDN:AAA41518.1, PID:g205154, release

A:Accession: B29450

A:Molecule type: mRNA

A:Residues: 19-30,122-218 <BAR2>

A:Cross-references: GB:M25821; GB:M24611; NID:g205155; PIDN:AAA41519.1; PID:g205156; GE

A:Experimental source: splice form 2

A:Accession: C29450

A:Molecule type: mRNA

A:Residues: 20-30,73-121,163-218 <BAR3>

A:Cross-references: GB:M25822; GB:M24611; NID:g205157; PIDN:AAA41520.1; PID:g205158; GE

A:Experimental source: splice form 3

A:Accession: D29450

A:Molecule type: mRNA

A:Residues: 28-218 <BAR4>

A:Cross-references: GB:M25823; GB:M24611; NID:g205159; PIDN:AAA41521.1; PID:g205160; GE

A:Experimental source: splice form 4

A>Note: the sequence in GenBank entry RATLCAIV, release 113.0, has the codon AGG for 56  
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

Adv. Exp. Med. Biol. 237, 3-7, 1988

A:Title: The leukocyte-common antigen (L-CA) family.

A:Reference number: A60241; MUID:89319817; PMID:2578200

A:Accession: A60241

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 30-161 <BAR5>

R:Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.



Cell 41, 83-93, 1985  
A:Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans the  
A:Reference number: A02247; MUID:85201691; PMID:3158393  
A:Accession: A02247  
A:Molecule type: mRNA  
A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>  
A:Cross-references: GB:M10072; GB:M81859; NID:G205140; PIDN:AAA41513.1; PID:G205143  
A:Note: The translation in GenBank entry RAYLCA1, release 113.0, begins at non-initiated  
A:Note: parts of this sequence were determined by protein sequencing  
R:McCall, M.N.; Shotton, D.M.; Barclay, A.N.  
Immunology 76, 310-317, 1992  
A:Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and  
A:Reference number: I54569; MUID:92340120; PMID:1378817  
A:Accession: I54569  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-30, 163-180 <MCC>  
A:Cross-references: GB:S40716; NID:G252015; PIDN:AA22648.1; PID:G252016  
R:Jackson, D.I.; Barclay, A.N.  
Immunogenetics 29, 281-287, 1989  
A:Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are derived  
A:Reference number: A45854; MUID:89233293; PMID:2523868  
A:Accession: A45854  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>  
A:Cross-references: GB:M18347; GB:M18348; GB:M18349  
C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.  
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolog  
F:1-23/Domain: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric  
F:24-1273/Domain: signal sequence #status predicted <SIG>  
F:24-546/Domain: leukocyte common antigen precursor, splice form 4 #status predicted <EXT>  
F:24-30, 122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MCC>  
F:24-30, 163-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MCC>  
F:24-30, 121-163-218/Product: leukocyte common antigen, splice form 3 #status predicted <MCC>  
F:547-568/Domain: transmembrane #status predicted <TM>  
F:565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:569-1273/Domain: intracellular #status predicted <INT>  
F:646-870/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:62, 142, 153, 164, 178, 200, 245, 271, 282, 327, 371, 374, 502/Binding site: carbohydrate (Asn) (C  
F:822/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F:828/Binding site: substrate phosphate (Arg) #status predicted  
F:1063/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 2.7%; Score 11; DB 1; Length 1273;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCASGVGRTG 367  
|||||  
Db 820 VHCASGVGRTG 830

RESULT 55  
A28334  
protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse  
N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); P  
N:Contents: protein-tyrosine-phosphatase (T-cell variant)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jun-2002  
C:Accession: A28334; A29381; A61180; A60933; A33522; A29075; I54450; A28335; I5  
R:Thomas, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987  
A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.  
A:Reference number: A28334; MUID:87260386; PMID:2955416  
A:Accession: A28334  
A:Molecule type: mRNA  
A:Residues: 1-1291 <THO>  
A:Cross-references: GB:M22455  
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986  
A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.

A:Reference number: A29381; MUID:86313686; PMID:2944116  
A:Accession: A29381  
A:Molecule type: mRNA  
A:Residues: 1-30, 170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930,  
A:Cross-references: GB:M14342; NID:G198914; PIDN:AAA39458.1; PID:G198915  
R:Yi, T.; Cleveland, J.L.; Ihle, J.N.  
Blood 78, 2222-2228, 1991  
A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells  
A:Reference number: A61180; MUID:92032882; PMID:1932742  
A:Accession: A61180  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 730-838 <YIA>  
R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.  
Immunogenetics 25, 263-266, 1987  
A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte comm  
A:Reference number: A60933; MUID:87192931; PMID:3570377  
A:Accession: A60933  
A:Molecule type: protein  
A:Residues: 'R', 289-298, 329, 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375, 595-608, 638-649, 66;  
R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.  
J. Biol. Chem. 264, 6220-6229, 1989  
A:Title: Sequence conservation in potential regulatory regions of the mouse and human  
A:Reference number: A33522; MUID:89197920; PMID:2522330  
A:Accession: A33522  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <JOH>  
A:Cross-references: GB:M22456; NID:G198755; PIDN:AAA46374.1; PID:G554185; GB:J04640; G  
R:Raschke, W.C.  
Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987  
A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-  
A:Reference number: A29075; MUID:87092355; PMID:2948186  
A:Accession: A29075  
A:Molecule type: mRNA  
A:Residues: 961-1291 <RAS>  
A:Cross-references: GB:M15174; NID:G201105; PIDN:AAA40161.1; PID:G201106  
R:Tung, J.  
Immunogenetics 28, 271-277, 1988  
A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in otl  
A:Reference number: I54450; MUID:88330145; PMID:3417340  
A:Accession: I54450  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 32-73 <RES>  
A:Cross-references: GB:M23241; NID:G340850; PIDN:AAA39460.1; PID:G548174  
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987  
A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguish:  
A:Reference number: A28335; MUID:87260987; PMID:3037546  
A:Accession: A28335  
A:Molecule type: mRNA  
A:Residues: 1-30, 74-226 <SA2>  
A:Cross-references: GB:M14342  
R:Shen, F.W.; Saga, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985  
A:Reference number: A23329; MUID:86042665; PMID:3864163  
A:Accession: A23329  
A:Molecule type: mRNA  
A:Residues: 10-30, 170-263 <SHS>  
A:Cross-references: GB:M1934; NID:G198919; PIDN:AAA39461.1; PID:G198920  
R:Saga, Y.; Tung, J.  
Mol. Cell. Biol. 8, 4889-4895, 1988  
A:Title: Organization of the Ly-5 Gene.  
A:Reference number: I57644; MUID:89056862; PMID:3211131  
A:Accession: I57644  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 'R', 1-22 <RE2>  
A:Cross-references: GB:M23354; NID:G340890; PIDN:AAA39462.1; PID:G554192  
C:Genetics:  
A:Gene: Ly-5  
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain hom

Query Match 2.7%; Score 11; DB 1; Length 1301;  
Best Local Similarity 100.0%; Pred.No. 0.02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHC5AGVGRGTG 367  
|||||  
DB 680 VHC5AGVGRGTG 690

RESULT 57  
A46546  
leukocyte common antigen long splice form precursor - human  
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprotein  
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000  
C:Accession: A46546; B46546; C46546; A29449; B29449; I57658  
R:Streuli, M.; Hall, L.R.; Sago, Y.; Schlossman, S.F.; Saito, H.  
J Exp. Med 166, 1548-1566, 1987  
A:Title: Differential usage of three exons generates at least five different mRNAs encoding  
A:Reference number: A46546; MUID:88061067; PMID:2824653  
A:Accession: A46546  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1304 <STR>  
A:Cross-references: GB:Y00638  
A:Experimental source: clone LCA. 6/2  
A:Accession: B46546  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-32,99-264 <ST2>  
A:Cross-references: GB:Y00638  
A:Experimental source: clone LCA.111 and clone LCA.260  
A:Accession: C46546  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-31,193-264 <ST3>  
A:Cross-references: GB:Y00638  
A:Experimental source: clone LCA.1  
R:Kaigh, S.O.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.  
EMBO J. 6, 1251-1257, 1987  
A:Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).  
A:Reference number: A91066; MUID:87275816; PMID:2956090  
A:Accession: A29449  
A:Molecule type: mRNA  
A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>  
A:Cross-references: GB:Y00662; NID:G34275; PIDN:CBA68269.1; PID:G34276  
A:Experimental source: clones pHLc-1 and lambdaHUG1  
A:Accession: B29449  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 32-192 <RA2>  
A:Experimental source: clone HLC-2  
R:Tsay, A.Y.; Streuli, M.; Saito, H.  
Mol. Cell. Biol. 9, 4550-4555, 1989  
A:Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative  
A:Reference number: I57658; MUID:90066468; PMID:2531281  
A:Accession: I57658  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 146-192 <RES>  
A:Cross-references: GB:M29253; NID:gi87020; PIDN:AAA59497.1; PID:G553521  
C:Genetics:  
A:Gene: GDB:PTPRC; CD45  
A:Cross-references: GDB:119768; OMIM:151460  
A:Map position: 1q31-1q32  
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolog  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydrolase  
F:1675-899/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1675-899/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:851/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 1304;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
DB 849 VHCAGVGRGTG 859  
|||||

RESULT 58  
T42636  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 17-Mar-2000  
C:Accession: T42636  
R:Qinghua, X.; Xiaojun, G.; Cong, S.; Zong, S.M.; Jong, Y.J.; Chan, J.; Wang, L.H.  
submitted to the EMBL Data Library, October 1995  
A:Reference number: Z22226  
A:Accession: T42636  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1422 <QIN>  
A:Cross-references: EMBL:U38349; NID:G1617477; PID:G1617478; PIDN:AAB16910.1  
A:Experimental source: kidney and brain  
C:Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase hom  
ne-phosphatase homology  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot

Query Match 2.7%; Score 11; DB 2; Length 1422;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
DB 1035 VHCAGVGRGTG 1045  
|||||

RESULT 59  
T31093  
probable protein-tyrosine-phosphatase (EC 3.1.3.48) - medicinal leech  
N:Alternate names: receptor tyrosine phosphatase  
C:Species: Hirudo medicinalis (medicinal leech)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T31093  
R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.  
submitted to the EMBL Data Library, December 1997  
A:Description: Two receptor tyrosine phosphatases expressed by neurons and muscle cells d  
A:Reference number: Z20976  
A:Accession: T31093  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1437 <GES>  
A:Cross-references: EMBL:AF017084; NID:G2695656; PID:G2695657; PIDN:AAB91461.1  
C:Genetics:  
A:Gene: LAR1  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
og  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

Query Match 2.7%; Score 11; DB 2; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPET 241  
DB 943 YIATQGLPET 953  
|||||

RESULT 60  
T19121  
probable protein-tyrosine-phosphatase (EC 3.1.3.48), receptor C09D8.1 - Caenorhabditis e  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000

C:Accession: T19121; T21940  
R:Coles, L.  
submitted to the EMBL Data Library, November 1994  
A:Reference number: Z19075  
A:Accession: T19121  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1585 <WIL>  
A:Cross-references: EMBL:Z46811; PIDN:CAA86842.1; GSPDB:GN00020; CESP:C09D8.1  
A:Experimental source: clone C09D8  
R:Swinburne, J.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z19490  
A:Accession: T21940  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1585 <WIL>  
A:Cross-references: EMBL:Z49938; PIDN:CAA90189.1; GSPDB:GN00020; CESP:C09D8.1  
A:Experimental source: Clone F38A3  
C:Genetics:  
A:Gene: CESP:C09D8.1  
A:Map position: 2  
A:Introns: 51/1; 67/3; 156/1; 227/1; 274/3; 311/3; 356/1; 459/1; 487/3; 546/3; 718/3;  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology  
og  
C:Keywords: phosphoric monoester hydrolase

Query Match 2.7%; Score 11; DB 2; Length 1585;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLPET 241  
DB 1100 YIATQGLPET 1110  
|||||

RESULT 61  
S12050  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
R:de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.  
PEBS Lett. 282, 285-288, 1991  
A:Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.  
A:Reference number: S15818; MUID:91243813; PMID:1645282  
A:Accession: S15818  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1872-1911, 'VHMVLQK' <VRI>  
A:Accession: S15819  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1872-1997 <VR2>  
C:Genetics:  
A:Gene: GDB:FTPRB; PTPB  
A:Cross-references: GDB:127352; OMIM:176882  
A:Map position: 12q15-12q21  
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III  
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; rece  
F;1-22/Domain: signal sequence #status predicted <Sig>  
F;23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted  
F;23-1625/Domain: extracellular #status predicted <EXT>  
F;1626-1642/Domain: transmembrane #status predicted <TMN>

F:1643-1997/Domain: intracellular #status predicted <INT>  
F:1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:1904/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F:1910/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.7%; Score 11; DB 1; Length 1997;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
Db 1902 VHCSAGVGRGTG 1912  
|||||

RESULT 62  
TPPLK  
protein-tyrosine-phosphatase (EC 3.1.3.48) DUAR precursor - fruit fly (Drosophila melanogaster)  
N:Alternate names: leukocyte antigen-related protein  
C:Species: Drosophila melanogaster  
C:Date: 14-Dec-1990 #sequence\_revision 02-May-1994 #text\_change 22-Jun-1999  
C:Accession: A36182  
R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989  
A:Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila  
A:Reference number: A36182; MUID:90046860; PMID:2554325  
A:Accession: A36182  
A:Molecule type: mRNA  
A:Residues: 1-2029 <STR>  
A:Cross-references: GB:M27700; NID:G157811; PIDN:AAA28668.1; PID:G157812  
C:Genetics:  
A:Gene: FlyBase:Lar  
A:Cross-references: FlyBase:FBgn0000464  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-2029/Product: leukocyte antigen-related protein #status predicted <MAT>  
F:33-1377/Domain: extracellular #status predicted <EXT>  
F:50-113/Domain: immunoglobulin homology <IMM1>  
F:154-211/Domain: immunoglobulin homology <IMM2>  
F:249-303/Domain: immunoglobulin homology <IMM3>  
F:321-401/Domain: fibronectin type III repeat homology <FN3A>  
F:416-502/Domain: fibronectin type III repeat homology <FN3B>  
F:514-599/Domain: fibronectin type III repeat homology <FN3C>  
F:610-699/Domain: fibronectin type III repeat homology <FN3D>  
F:708-802/Domain: fibronectin type III repeat homology <FN3E>  
F:811-896/Domain: fibronectin type III repeat homology <FN3F>  
F:909-993/Domain: fibronectin type III repeat homology <FN3G>  
F:1006-1091/Domain: fibronectin type III repeat homology <FN3H>  
F:1101-1198/Domain: fibronectin type III repeat homology <FN3I>  
F:1378-1402/Domain: transmembrane #status predicted <TM>  
F:1403-2029/Domain: intracellular #status predicted <INT>  
F:1497-1718/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP3>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP4>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP5>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP6>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP7>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP8>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP9>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP10>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP11>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP12>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP13>  
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F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP97>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP98>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP99>  
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP100>

```
Db      1930 VHCSAGVGRGTG 1940

RESULT 64
T34229
hypothetical protein F20B6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34229
R:Minx, P.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F20B6.
A:Reference number: Z21491
A:Accession: T34229
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <MIN>
A:Cross-references: EMBL:U41015; PIDN:AAA82310.1; CESP:F20B6.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F20B6.1
A:Introns: 24/2; 48/3; 108/2

Query Match      2.5%; Score 10; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      358 HCSAGVGRGTG 367
Db      114 HCSAGVGRGTG 123

RESULT 65
T21365
hypothetical protein F25H5.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21365
R:Steward, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19412
A:Accession: T21365
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-490 <WIL>
A:Cross-references: EMBL:Z81068; PIDN:CAB02988.1; GSPDB:GN000019; CESP:F25H5.7
A:Experimental source: clone F25H5
C:Genetics:
A:Gene: CESP:F25H5.7
A:Map position: 1
A:Introns: 32/3; 174/3; 390/1; 440/3; 473/2

Query Match      2.5%; Score 10; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCSAGVGRGT 366
Db      376 VHCSAGVGRGT 385

RESULT 66
T25430
hypothetical protein T28F4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25430
R:McMurray, A.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20033
A:Accession: T25430
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-490 <WIL>
A:Cross-references: EMBL:Z72517; PIDN:CAA96694.1; GSPDB:GN000019; CESP:T28F4.3
A:Experimental source: clone T28F4
C:Genetics:
A:Gene: CESP:T28F4.3
A:Map position: 1
A:Introns: 89/2; 206/2; 244/3; 403/3; 454/3

Query Match      2.5%; Score 10; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCSAGVGRGT 366
Db      252 VHCSAGVGRGT 261

RESULT 67
T29589
hypothetical protein F55F8.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29589
R:Gattung, S.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid F55F8.
A:Reference number: Z20647
A:Accession: T29589
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-518 <GAT>
A:Cross-references: EMBL:U80447; PIDN:AAB37811.1; GSPDB:GN000019; CESP:F55F8.7
A:Experimental source: strain Bristol N2; clone F55F8
C:Genetics:
A:Gene: CESP:F55F8.7
A:Map position: 1
A:Introns: 35/3; 175/3; 391/1; 441/3; 469/1

Query Match      2.5%; Score 10; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCSAGVGRGT 366
Db      377 VHCSAGVGRGT 386

RESULT 68
B87791
protein B0207.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B87791
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biol.
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_e
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a
A:Accession: B87791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-650 <STO>
A:Cross-references: GB:chr I; PIDN:AAB52456.1; PID:gl1943802; GSPDB:GN000019; CESP:B0207
A:Note: Similar to protein tyrosine phosphatase
C:Genetics:
A:Gene: B0207.1
A:Map position: 1

Query Match      2.5%; Score 10; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 358 HCSAGVGRG 367  
 |||||  
 Db 547 HCSAGVGRG 556

## RESULT 69

T42522  
 protein-tyrosine-phosphatase (EC 3.1.3.48) c1r-1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T42522; T42533  
 R:Kokel, M.; Borland, C.Z.; DeLong, L.; Horvitz, H.R.; Stern, M.J.  
 Genes Dev. 12, 1425-1437, 1998  
 A:Title: C1r-1 encodes a receptor tyrosine phosphatase that negatively regulates an FGF  
 A:Reference number: Z22170; MUID:98252828; PMID:9585503  
 A:Accession: T42522  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1409 <KOK>  
 A:Cross-references: EMBL:AF047880; NID:G3342254; PIDN:AA27551.1; PID:G3342255  
 A:Accession: T42533  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-940, 'IM' <KO2>  
 A:Cross-references: EMBL:AF047881; NID:G3342256; PIDN:AA27552.1; PID:G3342257  
 C:Genetics:  
 A:Gene: c1r-1  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 QY

## Query Match

Best Local Similarity 2.5%; Score 10; DB 2; Length 1409;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 HCSAGVGRG 367  
 |||||  
 Db 1012 HCSAGVGRG 1021

## RESULT 70

S51687  
 protein-tyrosine-phosphatase (EC 3.1.3.48), probable receptor type OST - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 23-Jul-1999  
 C:Accession: S51687

R:Celler, J.W.  
 submitted to the EMBL Data Library, September 1994

A:Reference number: S51687  
 A:Accession: S51687  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <CEL>

A:Cross-references: EMBL:X82004; NID:G603995; PIDN:CAA57530.1; PID:G603996  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III repeat  
 C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F.1-108/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>

## Query Match

Best Local Similarity 2.2%; Score 9; DB 2; Length 108;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVG 364  
 |||||  
 Db 91 LVHCSAGVG 99

## RESULT 71

T29155  
 hypothetical protein F47B3.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T29155  
 R:Du, Z.; Le, T.T.

submitted to the EMBL Data Library, April 1997  
 A:Description: The sequence of C. elegans cosmid F47B3.

A:Reference number: Z20579  
 A:Accession: T29155  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-130 <DUZ>  
 A:Cross-references: EMBL:U97017; PIDN:AAB52357.1; GSPDB:GN00019; CESP:F47B3.2  
 A:Experimental source: strain Bristol N2; clone F47B3  
 C:Genetics:  
 A:Gene: CESP:F47B3.2  
 A:Map position: 1  
 A:Introns: 4/3; 44/3; 69/3

## Query Match

Best Local Similarity 2.2%; Score 9; DB 2; Length 130;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGR 365  
 |||||  
 Db 19 VHCAGVGR 27

## RESULT 72

T46903  
 hypothetical protein DKFZp761A0712.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 02-Sep-2000  
 C:Accession: T46903  
 R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Weil, B.; Wiemann, S.  
 submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24134  
 A:Accession: T46903  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-248 <AAA>

A:Cross-references: EMBL:AL157451  
 A:Experimental source: adult amygdala; clone DKFZp761A0712  
 C:Genetics:  
 A:Note: DKFZp761A0712.1  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphat

## Query Match

Best Local Similarity 2.2%; Score 9; DB 2; Length 248;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGRLP 239  
 |||||  
 Db 49 YIATQGRLP 57

## RESULT 73

T29154  
 hypothetical protein F47B3.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T29154  
 R:Du, Z.; Le, T.T.  
 submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid F47B3.  
 A:Reference number: Z20579  
 A:Accession: T29154  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-374 <DUZ>

A:Cross-references: EMBL:U97017; PIDN:AAB52362.1; GSPDB:GN00019; CESP:F47B3.7  
 A:Experimental source: strain Bristol N2; clone F47B3  
 C:Genetics:  
 A:Gene: CESP:F47B3.7  
 A:Map position: 1  
 A:Introns: 52/3; 95/2; 248/3; 288/3; 313/3

## Query Match

Best Local Similarity 2.2%; Score 9; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGR 365  
|||  
DB 263 VHCAGVGR 271

RESULT 74  
A33939  
Fc gamma (IgG) receptor II precursor - Streptococcus sp. (fragment)  
C:Species: Streptococcus sp.  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 26-Aug-1999  
C:Accession: A33939  
R:Heath, D.G.; Cleary, P.P.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4741-4745, 1989  
A:Title: Fc-receptor and M-protein genes of group A streptococci are products of gene du  
A:Reference number: A33939; MUID:89282846; PMID:2660147  
A:Accession: A33939  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-405 <HEA>  
A:Cross-references: GB:M22532; NID:G153628; PIDN:AAB95296.1; PID:G552003  
C:Superfamily: M5 protein  
C:Keywords: immunoglobulin receptor

Query Match 2.2%; Score 9; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 0.76;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TLQKKEELD 164  
|||  
DB 99 TLQKKEELD 107

RESULT 75  
B53978  
protein-tyrosine-phosphatase (EC 3.1.1.3.48), nonreceptor type PTPX10 - African clawed fro  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 25-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 22-Jun-1999  
C:Accession: B53978  
R:Del Vecchio, R.L.; Tonks, N.K.  
J. Biol. Chem. 269, 19639-19645, 1994  
A:Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph  
A:Reference number: A53978; MUID:94308257; PMID:8034733  
A:Accession: B53978  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-597 <DEL>  
A:Cross-references: GB:L33099; NID:G495671; PIDN:AAA21728.1; PID:G495672  
A:Experimental source: ovary  
A:Note: sequence extracted from NCBI backbone (NCBIN:149759, NCBI:P:149760)  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas  
F:38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>  
F:328-564/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:516/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:522/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 9; DB 2; Length 597;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGLP 239  
|||  
DB 373 YIATQGLP 381

Search completed: June 21, 2004, 17:20:42  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 17:18:32 ; Search time 17 seconds  
(without alignments)  
1240.495 Million cell updates/sec

Title: US-09-095-478a-7

Perfect score: 405

Sequence: 1 MSSPRKVRGKTGRDNDEEG.....DIMNVITQMRKORCGMIQPK 405

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	3.7	1174	1 PPNL HUMAN	Q16825 homo sapien
2	15	3.7	1175	1 PPNL RAT	Q62728 rattus norv
3	15	3.7	1176	1 PPNL MOUSE	Q62136 mus musculus
4	14	3.5	1897	1 PTPF HUMAN	P10586 homo sapien
5	14	3.5	1912	1 PTPD HUMAN	P23468 homo sapien
6	14	3.5	1948	1 PTPN HUMAN	Q13332 homo sapien
7	12	3.0	1187	1 PTPN HUMAN	Q15878 homo sapien
8	12	3.0	1189	1 PTPN MOUSE	Q62130 mus musculus
9	12	3.0	1238	1 PTPJ HUMAN	Q64455 mus musculus
10	12	3.0	1337	1 PTPJ HUMAN	Q12913 homo sapien
11	12	3.0	1442	1 PTPG MOUSE	Q05909 mus musculus
12	12	3.0	1445	1 PTPG HUMAN	P23470 homo sapien
13	12	3.0	1462	1 PTP6 DROME	P16620 drosophila
14	12	3.0	1705	1 PTPV MOUSE	P70289 mus musculus
15	12	3.0	1711	1 PTPV RAT	Q64612 rattus norv
16	11	2.7	335	1 PTP1 YEAST	P25044 saccharomyc
17	11	2.7	521	1 PTP1 DICTDI	P34137 dictyosteli
18	11	2.7	550	1 PVP1 SCHPO	P27574 schizosacch
19	11	2.7	699	1 PTP6 MOUSE	P49446 mus musculus
20	11	2.7	700	1 PTP6 HUMAN	P23469 homo sapien
21	11	2.7	711	1 PTP2 SCHPO	P32586 schizosacch
22	11	2.7	796	1 PTRA RAT	Q03348 rattus norv
23	11	2.7	802	1 PTRA HUMAN	P18433 homo sapien
24	11	2.7	829	1 PTRA MOUSE	P18052 mus musculus
25	11	2.7	1152	1 CD45 MOUSE	P06800 mus musculus
26	11	2.7	1216	1 PTPO HUMAN	P16827 homo sapien
27	11	2.7	1255	1 CD45 RAT	P04157 rattus norv
28	11	2.7	1301	1 PTP9 DROME	P35322 drosophila
29	11	2.7	1304	1 CD45 HUMAN	P08575 homo sapien
30	11	2.7	1422	1 PTPG CHICK	Q98936 gallus gall
31	11	2.7	1997	1 PTPB HUMAN	P23467 homo sapien
32	11	2.7	2029	1 LAR DROME	P16621 drosophila
33	11	2.7	2200	1 LAR_CABEL	Q9bmm8 caenorhabdi

1	PTP2_HUMAN	2314	2.7	11	34
1	PTP2_RAT	2316	2.7	11	35
1	PTN1_HUMAN	458	2.2	9	36
1	PTP2_YEAST	750	2.2	9	37
1	PTN3_HUMAN	913	2.2	9	38
1	PTPX_MOUSE	1001	2.2	9	39
1	PTPX_RAT	1004	2.2	9	40
1	PTPX_MACNE	1013	2.2	9	41
1	PTPX_HUMAN	1015	2.2	9	42
1	PTP1_DROME	1631	2.2	9	43
1	PT25_STYPL	117	2.0	8	44
1	C114_MOUSE	573	2.0	8	45
1	PTN8_MOUSE	802	2.0	8	46
1	PTNM_HUMAN	807	2.0	8	47
1	PTPN_BOVIN	979	2.0	8	48
1	PTPN_MOUSE	979	2.0	8	49
1	PTPN_RAT	983	2.0	8	50
1	PT07_STYPL	112	1.7	7	51
1	CSF2_FELCA	144	1.7	7	52
1	S3DR_STAAM	180	1.7	7	53
1	S3DR_STAAM	180	1.7	7	54
1	Y4XK_RHISN	188	1.7	7	55
1	SPED_PSESM	264	1.7	7	56
1	Y149_MYCGE	281	1.7	7	57
1	END4_CHLAMU	288	1.7	7	58
1	YDRAO_HAEIN	313	1.7	7	59
1	DDLA_PSEPK	344	1.7	7	60
1	PTN7_RAT	352	1.7	7	61
1	PTN7_HUMAN	359	1.7	7	62
1	PTN5_RAT	369	1.7	7	63
1	PTP2_DICDI	377	1.7	7	64
1	DDL_STRAW	385	1.7	7	65
1	DDL_STROCO	389	1.7	7	66
1	BFTU_XYLF	395	1.7	7	67
1	G59F_DROME	406	1.7	7	68
1	PEPT_LACHE	413	1.7	7	69
1	VIAR_SHEEP	417	1.7	7	70
1	ECTB_MARHA	427	1.7	7	71
1	NORA_VIBHA	446	1.7	7	72
1	EFIA_ARATH	449	1.7	7	73
1	ARLY_OCEIH	459	1.7	7	74
1	ARLY_ANASP	461	1.7	7	75
1	ARLY_NOSPU	461	1.7	7	76
1	ARLY_CHLTE	463	1.7	7	77
1	ARLY_RHILLO	466	1.7	7	78
1	ARLY_CLOFE	466	1.7	7	79
1	ARLY_SYNP7	466	1.7	7	80
1	BDHR_HUMAN	477	1.7	7	81
1	Y4TO_RHISN	531	1.7	7	82
1	PTN5_HUMAN	541	1.7	7	83
1	PTN5_MOUSE	541	1.7	7	84
1	PTBP_ADR05	581	1.7	7	85
1	NUSM_XENLA	604	1.7	7	86
1	YOKG_YEAST	618	1.7	7	87
1	GLGB_COREF	731	1.7	7	88
1	PTN3_YEAST	926	1.7	7	89
1	UVRA_LISMO	956	1.7	7	90
1	BRD1_HUMAN	1058	1.7	7	91
1	BXCN_CLOBO	1196	1.7	7	92
1	SA3_MOUSE	1240	1.7	7	93
1	SA3_RAT	1256	1.7	7	94
1	APX_XENLA	1420	1.7	7	95
1	PTPK_HUMAN	1439	1.7	7	96
1	PTPM_HUMAN	1452	1.7	7	97
1	PTPM_HUMAN	1452	1.7	7	98
1	PTPM_HUMAN	1452	1.7	7	99
1	PTPM_HUMAN	1452	1.7	7	100

ALIGNMENTS

RESULT 1



```

PTNL_HUMAN
ID PTNL_HUMAN STANDARD; PRT; 1174 AA.
AC Q16825;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase D1).
GN PTPN21 OR PTPD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=94329538; PubMed=7519780;
RA Moeller N.P.H., Moeller K.B., Lammers R., Kharitonov A., Sures I.,
RA Ullrich A.;
RT "Src kinase associates with a member of a distinct subfamily of
RT protein-tyrosine phosphatases containing an ezrin-like domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7477-7481(1994).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X79510; CA56042.1; -.
DR PIR; I38140; I38140.
DR HSSP; Q06124; 2SHP.
DR Genew; HGNC:9651; PTPN21.
DR MIM; 603271; -.
DR GO; GO:0005856; C:cytoskeleton; TAS.
DR GO; GO:0004735; P:protein tyrosine phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00373; Band 4.1; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHTPASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS0057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
KW Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 23 308
FT ACT_SITE 921 1174
FT PROTEIN-TYROSINE PHOSPHATASE.
FT PHOSPHOCYSTEINE INTERMEDIATE
FT (BY SIMILARITY).
FT DOMAIN 340 343
FT DOMAIN 565 574
FT DOMAIN 712 717
FT POLY-PRO.
FT POLY-GLU.
SQ SEQUENCE 1174 AA; 133287 MW; 5772D9B1A99B3FDA CRC64;
Query Match 3.7%; Score 15; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 354 PLLVHCSAGVGRTGV 368
DB 1103 PLLVHCSAGVGRTGV 1117
|||||
RESULT 2
PTNL_RAT
ID PTNL_RAT STANDARD; PRT; 1175 AA.
AC Q62728; Q62732;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 2B).
GN PTPN21 OR PTP2E.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2B).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=9510449; PubMed=7805871;
RA L'Abbe D., Barville D., Tong Y., Stocco R., Masson S., Ma S.,
RA Fantus G., Shen S.H.;
RT "Identification of a novel protein tyrosine phosphatase with sequence
RT homology to the cytoskeletal proteins of the band 4.1 family.";
RL FEBS Lett. 356:351-356(1994).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q62728-1; Sequence=Displayed;
CC Name=2B;
CC IsoId=Q62728-2; Sequence=VSP_000498;
CC -!- TISSUE SPECIFICITY: Particularly abundantly in adrenal glands.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17971; AAA62153.1; -.
DR EMBL; U18293; AAA62154.1; -.
DR PIR; S51005; S51005.
DR HSSP; Q06124; 2SHP.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 4.1; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHTPASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS0057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
KW Structural protein; Cytoskeleton; Hydrolase; Alternative splicing.
FT DOMAIN 23 308
FT DOMAIN 922 1175
FT PROTEIN-TYROSINE PHOSPHATASE.
FT PHOSPHOCYSTEINE INTERMEDIATE
FT (BY SIMILARITY).
FT ACT_SITE 1109 1109

```

FT VARGPLIC 1 839 Missing (in isoform 2E).  
 FT /FTID=VSP\_000498  
 SQ SEQUENCE 1175 AA; 133411 MW; 82A682F1C0F5EC7 CRC64;

Query Match 3.7%; Score 15; DB 1; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCAGVGRTGV 368  
 |||||  
 DB 1104 PLLVHCAGVGRTGV 1118

## RESULT 3

PTNL\_MOUSE  
 ID PTNL\_MOUSE STANDARD; PRT; 1176 AA.  
 AC Q62136;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE (Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48))  
 GN PTPN21.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Liver;  
 RX MEDLINE=95140431; PubMed=7838537;  
 RA Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,  
 RA Takenawa J., Nakayama H., Fujita J.;  
 RT "Enhanced expression of multiple protein tyrosine phosphatases in the  
 RT regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-  
 RT type phosphatase with sequence homology to cytoskeletal protein  
 RT 4.1.1";  
 RL Oncogene 10:407-414(1995).  
 CC -1- FUNCTION: May be involved in the regulation of growth and  
 CC differentiation of liver cells.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC Non-receptor class subfamily.  
 CC -1- TISSUE SPECIFICITY: Liver.  
 CC -1- SIMILARITY: Contains 1 PTP domain.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.

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 -----

EMBL; D37801; BAA07053.1; -  
 PIR; I58345; I58345.  
 HSP; P29350; IGWZ.  
 DR MGP; MG1134406; Ptpn21.  
 DR InterPro; IPR000299; Band 4.1.  
 DR InterPro; IPR000387; Tyr\_PTPase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00373; Band 41; 1.  
 DR Pfam; PF00102; Y phosphatase; 1.  
 DR PRINTS; PR00935; BANDA41.  
 DR PRINTS; PR00700; PRTYPHTASE.  
 DR SMART; SM00295; B41; 1.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00660; FERM 1; 1.  
 DR PROSITE; PS00661; FERM 2; 1.  
 DR PROSITE; PS50057; FERM 3; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 KW Structural protein; Cytoskeleton; Hydrolase.  
 FT DOMAIN 23 308 FERM.  
 FT DOMAIN 923 1176 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1110 1110 PHOSPHOCYSTEINE INTERMEDIATE  
 (BY SIMILARITY).  
 FT DOMAIN 340 343 POLY-PRO.  
 FT DOMAIN 565 572 POLY-PRO.  
 SQ SEQUENCE 1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;

Query Match 3.7%; Score 15; DB 1; Length 1176;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCAGVGRTGV 368  
 |||||  
 DB 1105 PLLVHCAGVGRTGV 1119

## RESULT 4

PTPF\_HUMAN  
 ID PTPF\_HUMAN STANDARD; PRT; 1897 AA.  
 AC P10586;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).  
 GN PTPRF OR LAR.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tonsil;  
 RX MEDLINE=89035378; PubMed=2972792;  
 RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.P., Saito H.;  
 RT "A new member of the immunoglobulin superfamily that has a  
 RT cytoplasmic region homologous to the leukocyte common antigen.";  
 RL J. Exp. Med. 168:1523-1530(1988).  
 RN [2]  
 RP MUTAGENESIS.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 RT and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 RN [3]  
 RP MUTAGENESIS.  
 RX MEDLINE=90316093; PubMed=1695146;  
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;  
 RT "Distinct functional roles of the two intracellular phosphatase like  
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and  
 RT LAR.";  
 RL EMBO J. 9:2399-2407(1990).

CC -1- FUNCTION: It is possible that LAR is a cell adhesion receptor.  
 CC It possesses an intrinsic protein tyrosine phosphatase activity  
 CC (PTPase).  
 CC -1- FUNCTION: The first PTPase domain has enzymatic activity, while  
 CC the second one seems to affect the substrate specificity of the  
 CC first one.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -----  
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InterPro; IPR003961; FN III.  
 InterPro; IPR003962; FNIII subd.  
 InterPro; IPR007110; Ig-like.  
 InterPro; IPR003598; Ig\_c2.  
 InterPro; IPR000387; Tyr\_phosphatase.  
 InterPro; IPR000242; Tyr\_PP.  
 Pfam; PF00041; fn3; 8.  
 Pfam; PF00047; ig; 3.  
 Pfam; PF00102; Y\_phosphatase; 2.  
 PRINTS; PR00014; FNTYPELII.  
 PRINTS; PR00700; PRTYPHPTASE.  
 SMART; SM00408; IGC2; 3.  
 SMART; SM00194; PTPC; 2.  
 PROSITE; PS00835; IG LIKE; 3.  
 PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 PROSITE; PS00058; TYR\_PHOSPHATASE\_2; 2.  
 PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
 SIGNAL 1 29  
 CHAIN 30 1948  
 DOMAIN 30 1282  
 TRANSHEM 1283 1303  
 DOMAIN 1304 1948  
 DOMAIN 33 123  
 DOMAIN 135 233  
 DOMAIN 245 327  
 DOMAIN 329 422  
 DOMAIN 426 523  
 DOMAIN 525 615  
 DOMAIN 618 717  
 DOMAIN 720 831  
 DOMAIN 834 926  
 DOMAIN 928 1033  
 DOMAIN 1036 1151  
 DOMAIN 1193 1648  
 DOMAIN 180 1930  
 DOMAIN 641 644  
 DISULFID 54 107  
 DISULFID 156 216  
 DISULFID 266 311  
 ACT\_SITE 1589  
 ACT\_SITE 1880  
 CARBOHYD 263  
 CARBOHYD 308  
 CARBOHYD 733  
 CARBOHYD 940  
 VARSPLIC 190  
 VARSPLIC 236  
 VARSPLIC 617  
 VARSPLIC 784  
 VARSPLIC 1035  
 VARSPLIC 1350  
 VARSPLIC 1366  
 CONFLICT 310  
 CONFLICT 428  
 CONFLICT 742  
 CONFLICT 765  
 CONFLICT 910  
 CONFLICT 986  
 CONFLICT 1195  
 CONFLICT 1431

InterPro; IPR003961; FN III.  
 InterPro; IPR003962; FNIII subd.  
 InterPro; IPR007110; Ig-like.  
 InterPro; IPR003598; Ig\_c2.  
 InterPro; IPR000387; Tyr\_phosphatase.  
 InterPro; IPR000242; Tyr\_PP.  
 Pfam; PF00041; fn3; 8.  
 Pfam; PF00047; ig; 3.  
 Pfam; PF00102; Y\_phosphatase; 2.  
 PRINTS; PR00014; FNTYPELII.  
 PRINTS; PR00700; PRTYPHPTASE.  
 SMART; SM00408; IGC2; 3.  
 SMART; SM00194; PTPC; 2.  
 PROSITE; PS00835; IG LIKE; 3.  
 PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 PROSITE; PS00058; TYR\_PHOSPHATASE\_2; 2.  
 PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
 SIGNAL 1 29  
 CHAIN 30 1948  
 DOMAIN 30 1282  
 TRANSHEM 1283 1303  
 DOMAIN 1304 1948  
 DOMAIN 33 123  
 DOMAIN 135 233  
 DOMAIN 245 327  
 DOMAIN 329 422  
 DOMAIN 426 523  
 DOMAIN 525 615  
 DOMAIN 618 717  
 DOMAIN 720 831  
 DOMAIN 834 926  
 DOMAIN 928 1033  
 DOMAIN 1036 1151  
 DOMAIN 1193 1648  
 DOMAIN 180 1930  
 DOMAIN 641 644  
 DISULFID 54 107  
 DISULFID 156 216  
 DISULFID 266 311  
 ACT\_SITE 1589  
 ACT\_SITE 1880  
 CARBOHYD 263  
 CARBOHYD 308  
 CARBOHYD 733  
 CARBOHYD 940  
 VARSPLIC 190  
 VARSPLIC 236  
 VARSPLIC 617  
 VARSPLIC 784  
 VARSPLIC 1035  
 VARSPLIC 1350  
 VARSPLIC 1366  
 CONFLICT 310  
 CONFLICT 428  
 CONFLICT 742  
 CONFLICT 765  
 CONFLICT 910  
 CONFLICT 986  
 CONFLICT 1195  
 CONFLICT 1431

FT CONFLICT 1546 1546 E -> D (IN REF. 4).  
 FT CONFLICT 1587 1587 V -> A (IN REF. 4).  
 FT CONFLICT 1705 1705 N -> K (IN REF. 2).  
 SQ SEQUENCE 1948 AA; 217080 MW; 7DC049EC03171136 CRC64;  
 Query Match 3.5%; Score 14; DB 1; Length 1948;  
 Best Local Similarity 100.0%; Pred No. 4.2e-06; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0;  
 Qv 357 VHCAGVGRGTGVFI 370  
 |||||  
 Db 1878 VHCAGVGRGTGVFI 1891  
 RESULT 7  
 ID PTNE HUMAN STANDARD; PRT; 1187 AA.  
 AC Q15678;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)  
 DE RECEPTOR-TYPE PROTEIN-TYROSINE  
 GN PTN14 OR PEZ.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast carcinoma;  
 RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,  
 RA Crompton M.R.;  
 RA "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and  
 ezrin-like domains"; Commun. 209:959-965(1995).  
 RT Biochem. Biophys. Res. Commun. 209:959-965(1995).  
 RL -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- TISSUE SPECIFICITY: Expressed in a variety of human tissues  
 CC including kidney, skeletal muscle, lung and placenta.  
 CC -!- SIMILARITY: Contains 1 FERM domain.  
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC -----  
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 CC -----  
 CC EMBL; X82676; CAA57993.1; -.  
 DR PIR; JC4155; JC4155.  
 DR HSSP; P29350; 1GMZ.  
 DR Genew; HGNC:9647; PTPN14.  
 DR MIM; 603155;  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR InterPro; IPR00299; Band 4.1.  
 DR InterPro; IPR00387; TYR phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00373; Band 41; I.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00935; BAND41.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00295; B41; 1.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00660; FERM\_1; 1.  
 DR PROSITE; PS00661; FERM\_2; 1.  
 DR PROSITE; PS00057; FERM\_3; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE; PS0055; TYR PHOSPHATASE PTP; 1.  
 DR PROSITE; PS0057; TYR PHOSPHATASE 2; 1.  
 KW Structural protein; Cytoskeleton; Hydrolase.  
 FT DOMAIN 21 306 PERM.  
 FT ACT\_SITE 933 1167 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1121 1121 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).  
 FT DOMAIN 566 573 POLY-PRO.  
 FT DOMAIN 709 716 POLY-GLU.  
 SQ SEQUENCE 1187 AA; 135239 MW; 015760375B3574E3 CRC64;  
 Query Match 3.0%; Score 12; DB 1; Length 1187;  
 Best Local Similarity 100.0%; Pred. No. 0.00037;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGTG 368  
 DB 1119 VHCAGVGRGTG 1130  
 RESULT 8  
 PTNE\_MOUSE STANDARD; PRT; 1189 AA.  
 ID PTNE\_MOUSE STANDARD; PRT; 1189 AA.  
 AC Q62130;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase PTP36).  
 GN PTPN14  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CB-17-SCID; TISSUE=Thymus;  
 RX MEDLINE=94354845; PubMed=8074593;  
 RA Sawada M., Ogata M., Fujino Y., Kamaoka T.;  
 RT "CDNA cloning of a novel protein tyrosine phosphatase with homology  
 RT to cytoskeletal protein 4.1 and its expression in T-lineage cells.";  
 RL Biochem. Biophys. Res. Commun. 203:479-484(1994).  
 CC -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and  
 CC non-hematopoietic origins.  
 CC -!- SIMILARITY: Contains 1 FERM domain.  
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC  
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 CC  
 CC EMBL; D31842; BAA06628.1; -.  
 CC PIR; JC2366; JC2366.  
 CC HSSP; Q6124; 2SHP.  
 CC MGD; MGI:102467; Ptpn14.  
 CC InterPro; IPR000299; Tyr\_4.1.  
 CC InterPro; IPR000387; Tyr\_phosphatase.  
 CC InterPro; IPR00242; Tyr\_PP.  
 CC Pfam; PF00373; Band 41; I.  
 CC Pfam; PF00102; Y\_phosphatase; 1.  
 CC PRINTS; PR02935; BAND41.  
 CC PRINTS; PR00700; PTPPHPTASE.  
 CC SMART; SM00295; B41; 1.  
 CC SMART; SM00194; PTPC; 1.  
 CC PROSITE; PS00660; FERM\_1; 1.

DR PROSITE; PS00661; FERM 2; 1.  
 DR PROSITE; PS0057; FERM 3; 1.  
 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 1.  
 DR PROSITE; PS00055; TYR PHOSPHATASE PTP; 1.  
 DR PROSITE; PS00056; TYR PHOSPHATASE 2; 1.  
 KW Structural protein; Cytoskeleton; Hydrolase.  
 FT DOMAIN 21 306 PERM.  
 FT ACT\_SITE 935 1189 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1123 1123 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).  
 FT DOMAIN 566 573 POLY-PRO.  
 FT DOMAIN 635 639 POLY-GLY.  
 FT DOMAIN 712 718 POLY-GLU.  
 SQ SEQUENCE 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64;  
 Query Match 3.0%; Score 12; DB 1; Length 1189;  
 Best Local Similarity 100.0%; Pred. No. 0.00037;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGTG 368  
 DB 1121 VHCAGVGRGTG 1132  
 RESULT 9  
 PTPJ\_MOUSE STANDARD; PRT; 1238 AA.  
 ID PTPJ\_MOUSE STANDARD; PRT; 1238 AA.  
 AC Q64455;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)  
 DE (HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase  
 DE receptor type J) (Susceptibility to colon cancer-1).  
 GN PTPRJ OR BYP OR SCC1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MRL-LPR/LPR;  
 RX MEDLINE=96140699; PubMed=8549806;  
 RA Kuramochi S., Matsuda S., Matsuda Y., Saitoh T., Ohsugi M.,  
 RA Yamamoto T.;  
 RT Molecular cloning and characterization of ByP, a murine  
 RT receptor-type tyrosine phosphatase similar to human DEP-1.;  
 RL FEBS Lett. 378:7-14(1996).  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in every tissue examined.  
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC -!- SIMILARITY: Contains 6 fibronectin type III domains.  
 CC  
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 CC  
 CC EMBL; D45212; BAA08146.1; -.  
 CC PIR; S68700; S68700.  
 CC HSSP; P18052; 1YFO.  
 CC MGD; MGI:104574; Ptpnj.  
 CC GO; GO:0007507; P.heart development; IMP.  
 CC GO; GO:0001570; P.vasculogenesis; IMP.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003961; FN\_III.  
 CC InterPro; IPR000387; Tyr\_phosphatase.  
 CC InterPro; IPR000242; Tyr\_PP.

DR Pfam: PF00041; fn3, 6.  
 DR Pfam: PF00102; Y-phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3, 6.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Signal: Glycoprotein; Transmembrane; Repeat; Hydrolase.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT CHAIN 29 1238 PROTEIN-TYROSINE PHOSPHATASE ETA.  
 FT DOMAIN 29 876 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 877 897 POTENTIAL.  
 FT DOMAIN 898 1238 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 121 260 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 268 348 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 356 434 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 442 518 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 529 608 FIBRONECTIN TYPE-III 5.  
 FT DOMAIN 608 1238 FIBRONECTIN TYPE-III 6.  
 FT DOMAIN 966 1238 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT SITE 1140 1140 PHOSPHOCYSTEINE INTERMEDIATES (BY SIMILARITY).  
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 506 506 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 662 662 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 685 685 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 691 691 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 838 838 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1238 AA; 136782 MW; 959479EDC8016835 CRC64;

Query Match 3.0%; Score 12; DB 1; Length 1238;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 |||||  
 Db 1137 LVHCSAGVGRGTG 1148

RESULT 10  
 PTPJ\_HUMAN

ID PTPJ\_HUMAN STANDARD; PRT; 1337 AA.  
 AC Q12913; Q15255; Q8NEM2;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)  
 DE (HPTP eta) (protein-tyrosine phosphatase receptor type U) (Density  
 DE enhanced phosphatase-1) (DEP-1) (CD148 antigen).  
 GN PTPRJ OR DEPI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=95024024; PubMed=7937872;  
 RA Oestman A., Yang Q., Tonks N.K.;  
 RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,  
 RT is enhanced with increasing cell density.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95086212; PubMed=7994032;  
 RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;  
 RT "Molecular cloning, characterization, and chromosomal localization of  
 RT a novel protein-tyrosine phosphatase, HPTP eta.";  
 RL Blood 84:4186-4194(1994).  
 RN [3]  
 RP SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER CYS-214 AND  
 RP PRO-276.  
 RC TISSUE=Colon;  
 RX MEDLINE=22084388; PubMed=12089527;  
 RA Ruivenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vlcek C.,  
 RA Csikos T., Klaus A.M., Tripodis N., Petrakis A., Boerigter L.,  
 RA Groot P.C., Lindeman J., Mooi W.J., Meijer G.A., Scholten G.,  
 RA Daterse H., Paces V., van Zandwijk N., van Ommen G.J.B., Demant P.;  
 RT "Ptpj is a candidate for the mouse colon-cancer susceptibility locus  
 RT Sccl and is frequently deleted in human cancers.";  
 RL Nat. Genet. 31:295-300(2002).  
 CC -!- FUNCTION: May contribute to the mechanism of contact inhibition of  
 CC cell growth.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- PM: N- and O-glycosylated.  
 CC -!- DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and  
 CC breast.  
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC -!- SIMILARITY: Contains 5 fibronectin type III domains.  
 CC -!- DATABASE: RAMS-PROV; NOTE=CD guide CD148 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd148.htm".  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U10886; AAB36687.1; -;  
 DR EMBL; D37781; BAA07035.1; -;  
 DR EMBL; AF387844; AAM69432.1; -;  
 DR EMBL; AF387823; AAM69432.1; JOINED.  
 DR EMBL; AF387824; AAM69432.1; JOINED.  
 DR EMBL; AF387825; AAM69432.1; JOINED.  
 DR EMBL; AF387826; AAM69432.1; JOINED.  
 DR EMBL; AF387827; AAM69432.1; JOINED.  
 DR EMBL; AF387828; AAM69432.1; JOINED.  
 DR EMBL; AF387829; AAM69432.1; JOINED.  
 DR EMBL; AF387830; AAM69432.1; JOINED.  
 DR EMBL; AF387831; AAM69432.1; JOINED.  
 DR EMBL; AF387832; AAM69432.1; JOINED.

DR EMBL; AF387833; AAM69432.1; JOINED.  
 DR EMBL; AF387834; AAM69432.1; JOINED.  
 DR EMBL; AF387835; AAM69432.1; JOINED.  
 DR EMBL; AF387836; AAM69432.1; JOINED.  
 DR EMBL; AF387837; AAM69432.1; JOINED.  
 DR EMBL; AF387838; AAM69432.1; JOINED.  
 DR EMBL; AF387839; AAM69432.1; JOINED.  
 DR EMBL; AF387840; AAM69432.1; JOINED.  
 DR EMBL; AF387841; AAM69432.1; JOINED.  
 DR EMBL; AF387842; AAM69432.1; JOINED.  
 DR EMBL; AF387843; AAM69432.1; JOINED.  
 DR HSP; P18052; 11FO.  
 DR MIM; 600925; .  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. .; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.  
 DR InterPro; IPR009357; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR000387; Tyr\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 6.  
 DR PRINTS; PR00700; RTYPHPTASE.  
 DR SMART; SM00060; FN3; 8.  
 DR SMART; SM00194; PTP; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase;  
 Disease mutation.  
 FT SIGNAL 1 35 POTENTIAL.  
 FT CHAIN 36 1337 PROTEIN-TYROSINE PHOSPHATASE ETA.  
 FT DOMAIN 36 975 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 976 996 POTENTIAL.  
 FT DOMAIN 997 1337 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 119 199 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 366 446 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 454 532 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 604 615 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 626 710 FIBRONECTIN TYPE-III 5.  
 FT DOMAIN 1065 1337 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1239 1239 PHOSPHOTRANSFER INTERMEDIATE (BY SIMILARITY).  
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 525 525 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 536 536 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 582 582 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 666 666 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 669 669 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 761 761 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 772 772 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 784 784 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 790 790 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 824 824 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 910 910 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 937 937 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT VARIANT 214 214 R -> C (in colon cancer; somatic mutation).  
 FT FTID=VAR 015905.  
 FT Q -> P (in colon cancer; somatic mutation).  
 FT FTID=VAR 015906.  
 FT G -> D (IN REF. 1).  
 FT YNGKLEPLGYSR -> LOWBAGTSGLLP (IN REF. 2).  
 SQ SEQUENCE 1337 AA; 145926 MW; 2675252104B6AFE CRC64;  
 Query Match 3.0%; Score 12; DB 1; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 0.00041;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 LVHCSAGVGRIG 367  
 DB 1236 LVHCSAGVGRIG 1247  
 RESULT 11  
 ID\_PTPG\_MOUSE STANDARD; PRT; 1442 AA.  
 AC Q05909;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).  
 DE gamma).  
 GN PTPRG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RX MEDLINE=93180796; PubMed=8382771;  
 RA Barnea G., Silvennoinen O., Shaanan B., Honegger A.M., Canoll P.D., D'Sustachio P., Morse B., Levy J.B., Laforgia S., Huebner K., Musacchio J.M., Sap J., Schlessinger J.;  
 RA "Identification of a carbonic anhydrase-like domain in the extracellular region of RPTP gamma defines a new subfamily of receptor tyrosine phosphatases.";  
 RL Mol. Cell. Biol. 13:1497-1506(1993).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -1- TISSUE SPECIFICITY: Detected in brain, lung, kidney, heart, liver, skeletal muscle, spleen and testes. It is developmentally regulated in the brain.  
 CC -1- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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 CC EMBL; L09562; AAA00022.1; .  
 CC PIR; B48148; B48148.  
 CC HSSP; P18052; 11FO.  
 CC MGD; MGI:97814; Ptprg.



DR InterPro: IPR001148; Euk Coanhd.  
 DR InterPro: IPR008957; FN III-like.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR000387; Tyr phosphatase.  
 DR InterPro: IPR000242; Tyr PP.  
 DR Pfam: PF00194; carb anhydase; 1.  
 DR Pfam: PF00041; fni; 1.  
 DR Pfam: PF00102; 1-phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR ProDom: PD000865; Euk Coanhd; 1.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR PHOSPHATASE 1; 1.  
 DR PROSITE: PS00384; TYR PHOSPHATASE 2; 2.  
 DR PROSITE: PS00385; TYR PHOSPHATASE 3; 3.  
 DR Glycoprotein; Transmembrane; Hydrolase; Repeat; Signal.  
 DR SIGNAL 1 19  
 DR CHAIN 20 1442  
 DR DOMAIN 20 733  
 DR TRANSMEM 734 759  
 DR TRANSMEM 760 1442  
 DR DOMAIN 56 322  
 DR DOMAIN 347 441  
 DR DOMAIN 866 1122  
 DR DOMAIN 1123 1442  
 DR ACT\_SITE 1057 1057  
 DR SITE 1348 1348  
 DR CARBOHYD 109 109  
 DR CARBOHYD 113 113  
 DR CARBOHYD 156 156  
 DR CARBOHYD 359 359  
 DR CARBOHYD 444 444  
 DR CARBOHYD 719 719  
 DR SEQUENCE 1442 AA; 161242 MW; 5887715568FBECD8 CRC64;  
 Query Match 3.0%; Score 12; DB 1; Length 1442;  
 Best Local Similarity 100.0%; Pred No. 0.00045;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 356 LVHCSAGVGRGT 367  
 Db 1054 LVHCSAGVGRGT 1065  
 RESULT 12  
 ID PTPG\_HUMAN STANDARD; PRT; 1445 AA.  
 AC P23470; Q15C23;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).  
 DB Gamma.  
 GN PTPRG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93180796; PubMed=832771;  
 RA Barnea G., Silvenoinen O., Shaan B., Honneger A.M., Canoll P.D.,  
 RA D'Eustachio P., Morse B., Levy J.B., Laforgia S., Huebner K.,  
 RA Musacchio J.M., Sap J., Schlessinger J.;  
 RT Identification of a carbonic anhydrase-like domain in the  
 RT extracellular region of RPTP gamma defines a new subfamily of  
 RT receptor tyrosine phosphatases.;  
 RL Mol. Cell. Biol. 13:1497-1506(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96429999; PubMed=8833149;  
 RA Kastury K., Ohta M., Lasota J., Moir D., Dorman T., Laforgia S.,  
 RA Druck T., Huebner K.;  
 RT "Structure of the human receptor tyrosine phosphatase gamma gene  
 RT (PTPRG) and relation to the familial RCC t(3;8) chromosome  
 RT translocation.";  
 RL Genomics 32:225-235(1996).  
 RN [3]  
 RP SEQUENCE OF 836-1445 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=9106018; PubMed=2170109;  
 RA Krueger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein  
 RT tyrosine phosphatases.";  
 RL EMBO J. 9:3241-3252(1990).  
 RN [4]  
 RP SEQUENCE OF 874-1118 AND 1175-1409 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90384936; PubMed=2169617;  
 RA Kaplan R., Morse B., Huebner K., Croce C., Hawk R., Ravera M.,  
 RA Ricca G., Jaye M., Schlessinger J.;  
 RT "Cloning of three human tyrosine phosphatases reveals a multigene  
 RT family of receptor-linked protein-tyrosine-phosphatases expressed in  
 RT brain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: Found in a variety of tissues. It is  
 CC developmentally regulated in the brain (by similarity).  
 CC -!- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
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 DR EMBL; L09247; AAA60224.1;  
 DR EMBL; U46116; AAC50439.1;  
 DR EMBL; U46089; AAC50439.1; JOINED.  
 DR EMBL; U46090; AAC50439.1; JOINED.  
 DR EMBL; U46091; AAC50439.1; JOINED.  
 DR EMBL; U46092; AAC50439.1; JOINED.  
 DR EMBL; U46093; AAC50439.1; JOINED.  
 DR EMBL; U46094; AAC50439.1; JOINED.  
 DR EMBL; U46095; AAC50439.1; JOINED.  
 DR EMBL; U46096; AAC50439.1; JOINED.  
 DR EMBL; U46097; AAC50439.1; JOINED.  
 DR EMBL; U46098; AAC50439.1; JOINED.  
 DR EMBL; U46099; AAC50439.1; JOINED.  
 DR EMBL; U46100; AAC50439.1; JOINED.  
 DR EMBL; U46101; AAC50439.1; JOINED.  
 DR EMBL; U46102; AAC50439.1; JOINED.  
 DR EMBL; U46103; AAC50439.1; JOINED.  
 DR EMBL; U46104; AAC50439.1; JOINED.  
 DR EMBL; U46105; AAC50439.1; JOINED.  
 DR EMBL; U46106; AAC50439.1; JOINED.  
 DR EMBL; U46107; AAC50439.1; JOINED.  
 DR EMBL; U46108; AAC50439.1; JOINED.  
 DR EMBL; U46109; AAC50439.1; JOINED.  
 DR EMBL; U46110; AAC50439.1; JOINED.  
 DR EMBL; U46111; AAC50439.1; JOINED.  
 DR EMBL; U46112; AAC50439.1; JOINED.  
 DR EMBL; U46113; AAC50439.1; JOINED.  
 DR EMBL; U46114; AAC50439.1; JOINED.  
 DR EMBL; U46115; AAC50439.1; JOINED.  
 DR EMBL; X54132; CAA38067.1;  
 DR PIR; A48148; A48148.  
 DR HSSP; P18052; 1YFO.  
 DR Genew; HGNC:9671; PTPRG.

SEQUENCE FROM NP A.

MEDLINE=90046860; PubMed=2554325;

Streuli M., Krueger N.X., Isai A.Y.M., Saito H.;

"A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";

Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).

-1- FUNCTION: It is possible that DPTP is a cell adhesion receptor.

-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

-1- SIMILARITY: Contains 2 fibronectin type III domains.

-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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EMBL; M27699; AAA28842.1; --

PIR; B36182; B36182.

HSSP; P18052; IYFO.

FLYBase; FBgn0014007; Ptp69D.

GO; GO:0004725; P:protein tyrosine phosphatase activity; IDA.

GO; GO:0007415; P:defasciculation of motor neuron; IGI.

GO; GO:0008045; P:motor axon guidance; IGI.

GO; GO:0008470; P:protein amino acid dephosphorylation; IDA.

InterPro; IPR008957; FN\_III-like.

InterPro; IPR003961; FN\_III.

InterPro; IPR007110; IG-like.

InterPro; IPR003598; Ig\_c2.

InterPro; IPR000387; TYR\_phosphatase.

InterPro; IPR000242; Tyr\_PP.

Pfam; PF00041; fn3, 3.

Pfam; PF00047; Ig; 2.

Pfam; PF00102; Y\_phosphatase; 2.

PRINTS; PR00700; PRTPHPTASE.

SMART; SM00060; FN3; 3.

SMART; SM00408; IGC2; 1.

SMART; SM00194; PTPc; 2.

PROSITE; PS50835; IG\_LIKE; 2.

PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.

PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.

PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.

Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;

Cell adhesion; Immunoglobulin domain; Repeat.

FT SIGNAL 1 23

FT CHAIN 24 1462

FT DOMAIN 24 805

FT TRANSMEM 806 823

FT DOMAIN 824 1462

FT DOMAIN 24 125

FT DOMAIN 131 230

FT DOMAIN 332 437

FT DOMAIN 438 538

FT DOMAIN 912 1165

FT DOMAIN 1208 1459

FT ACT\_SITE 1097 1097

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 119 119

FT ACT\_SITE 1391 1391

FT DISULFID 45 112

FT DISULFID 154 214

FT CARBOHYD 40 40

FT CARBOHYD 58 58

FT CARBOHYD 64 64

FT CARBOHYD 85 85

FT CARBOHYD 105 105

FT CARBOHYD 109 109

FT CARBOHYD 1

[illegible]

DE (Embryonic stem cell protein-tyrosine phosphatase) (ES cell  
 OE phosphatase) (Osteostic protein-tyrosine phosphatase) (OST-PTP).  
 EN PTPV OR ESP.  
 OS Rattus norvegicus [Rat].  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Osteosarcoma;  
 RX MEDLINE=95074080; PubMed=7527035;  
 RA Mauro L.J., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R.,  
 RA Dixon J.E.,  
 RT "Identification of a hormonally regulated protein tyrosine  
 RT phosphatase associated with bone and testicular differentiation."  
 RE J. Biol. Chem. 269:30659-30667(1994).  
 CC -!- FUNCTION: May function in signaling pathways during bone  
 CC remodeling, as well as serve a broader role in cell interactions  
 CC associated with differentiation in bone and testis. Optimal pH for  
 CC phosphatase activity is 5.6. Associated with differentiation in  
 CC bone and testis.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=A presumed alternate transcript of 4.8-5.0 kilobases,  
 CC which may lack PTP domains, is present in proliferating  
 CC osteoblasts, but not detectable at other stages;  
 CC Name=1;  
 CC IsoId=Q64612-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q64612-2; Sequence=Not described;  
 CC Note=No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Bone and testis. In the latter, restricted to  
 CC the basal portion of the seminiferous tubule.  
 CC -!- DEVELOPMENTAL STAGE: Up-regulated in differentiating cultures of  
 CC primary osteoblasts and down-regulated in late stage mineralizing  
 CC cultures. In testis, expression is highest between stages I and  
 CC VII when maturing spermatids remain buried within the sertoli  
 CC epithelium.  
 CC -!- INDUCTION: By parathyroid hormone and cAMP analogs.  
 CC -!- PTM: The cytoplasmic domain contains potential phosphorylation  
 CC sites.  
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -!- SIMILARITY: Contains 10 fibronectin type III domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L36884; AAA63911.1; -;  
 DR HSP; P18052; 1VFO.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR000387; TYR\_Phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 7.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPTPHNTASE.  
 DR SMART; SM00060; FN3; 8.  
 DR SMART; SM00194; ETEC; 1.  
 DR PROSITE; PS00363; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KM Hydrolase; Transmembrane; Repeat; Signal; Glycoprotein;  
 KM Alternative splicing.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 1711 RECEPTOR-TYPE PROTEIN-TYROSINE

PT DOMAIN 18 1074 PHOSPHATASE V.  
 PT TRANSMEM 1075 1095 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1096 1711 POTENTIAL.  
 FT FIBRONECTIN TYPE-III 1. CYTOPLASMIC (POTENTIAL).  
 FT FIBRONECTIN TYPE-III 2. FIBRONECTIN TYPE-III 3. FIBRONECTIN TYPE-III 4. FIBRONECTIN TYPE-III 5. FIBRONECTIN TYPE-III 6. FIBRONECTIN TYPE-III 7. FIBRONECTIN TYPE-III 8. FIBRONECTIN TYPE-III 9. FIBRONECTIN TYPE-III 10. FIBRONECTIN TYPE-III 10. PROTEIN-TYROSINE PHOSPHATASE 1. PROTEIN-TYROSINE PHOSPHATASE 2. PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).  
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 737 737 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 851 851 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 970 970 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 982 982 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1711 AA; 187292 MW; 0F04D2D1A47A18A0 CRC64;  
 Query Match 3.0%; Score 12; DB 1; Length 1711;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 LVHCSAGVGRGTG 367  
 DB 1347 LVHCSAGVGRGTG 1358  
 RESULT 16  
 ID\_PTP1 YEAST STANDARD; PRT; 335 AA.  
 AC P25044;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase 1 (EC 3.1.3.48) (PTPase 1).  
 GN PTP1 OR YDL230W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91302312; PubMed=1649172;  
 RA Guan K., Deschenes R.J., Qiu H., Dixon J.E.;  
 RT "Cloning and expression of a yeast protein tyrosine phosphatase";  
 RL J. Biol. Chem. 266:12964-12970(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rasmussen S.W.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Is not required for vegetative growth.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

```

CC CC -!- MISCELLANEOUS: The PTPase domain is interrupted by a PTPase insert
CC CC which shares no homologies with other PTPase proteins.
CC CC
CC CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC CC Non-receptor class subfamily.
CC CC
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CC CC or send an email to license@isb-sib.ch)
CC CC
CC CC EMBL; L07125; AAA33241.1; -.
CC CC HSSP; Q06124; 2SHP.
CC CC
CC CC DictyBase; DBE0168065; ptpAL.
CC CC InterPro; IPR000387; TYR_phosphatase.
CC CC InterPro; IPR000242; TYR_PP.
CC CC Pfam; PF00102; Y_phosphatase; 1.
CC CC PRINTS; PR00700; PTYEPHPHASE.
CC CC SMART; SM00194; PTPC; 1.
CC CC PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
CC CC PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
CC CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC CC
CC KW Hydrolase.
CC
CC FT DOMAIN 1 114 SER-RICH
CC FT ACT_SITE 310 310 PHOSPHOCYSTEINE INTERMEDIATE (BY
CC FT SIMILARITY).
CC FT DOMAIN 327 425 PTPASE INSERT (ASN-RICH) .
CC FT DOMAIN 382 400 POLY-ASN.
CC FT SEQUENCE 521 AA; 59427 MW; 0F516AEDD075EAB96 CRC64;

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Query Match 2.7%; Score 11; DB 1; Length 521;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY		357	VHCSAGVGRTS	367
NB		398	VHCSPGVGRTC	318

RESULT 18	PPYL_SCHPO	STANDARD;	PRT;	550 AA.
ID	PPYL_SCHPO			
AC	P27574;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Protein-tyrosine phosphatase 1 (EC 3.1.3.48) (PTase 1).			
GN	PPYL OR SPAC26P1.10C.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			
NCBI	TaxID=4896;			
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=91195370; PubMed=1849659;			
RX	Orellis S., Chernoff J., Hannig G., Hoffman C.S., Erikson R.L.;			
RT	"A fission-yeast gene encoding a protein with features of protein-			
RT	tyrosine-phosphatases."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:3455-3459 (1991).			
[2]	SEQUENCE FROM N.A.			
RP	STRAIN=972;			
RC	MEDLINE=21848401; PubMed=11859360;			
RX	Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Sources J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLea J.,			

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymouprez B.,  
RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Carrutti I., Lowe T., McCombie W.B., Paulsen I., Potashkin J.,  
RA Szpakowski G.V., Ussery D., Barrell B.G., Nurse P.,  
RA Nature 415:871-880(2002).  
RL The genome sequence of Schizosaccharomyces pombe.;  
RN Nature 415:871-880(2002).  
RP CHARACTERIZATION.  
RX MEDLINE=93099859; PubMed=1464319;  
RA Millar J.B.A., Russell P., Dixon J.E., Guan K.L.;  
RT "Negative regulation of mitosis by two functionally overlapping  
RT PTPases in fission yeast.";  
RL EMBO J. 11:4943-4952(1992).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=95385997; PubMed=7657164;  
RA Millar J.B.A., Buck V., Wilkinson M.G.;  
RT "Fypl and Fyp2 PTPases dephosphorylate an osmosensing MAP kinase  
RT controlling cell size at division in fission yeast.";  
RL Genes Dev. 9:2117-2130(1995).  
CC -I- FUNCTION: Plays a role in inhibiting the onset of mitosis.  
CC Dephosphorylates sty1/spc1 and wis1/spc2/sty2.  
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
CC tyrosine + phosphate.  
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
CC Non-receptor class subfamily.  
CC  
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CC  
CC EMBL: M63257; AAA35328.1; -  
CC EMBL: Z73100; CAA97367.1; -  
CC PIR: A40449; A40449.  
CC HSSP: P18052; 1YFO.  
CC Gated SPombe; SPAC26F1.10c; -  
CC InterPro; IPR001763; Rhodanese-like.  
CC InterPro; IPR000387; Tyr phosphatase.  
CC InterPro; IPR000242; Tyr\_PP.  
CC Pfam; PF00581; Rhodanese\_1.  
CC Pfam; PF00102; Y\_phosphatase; 1.  
CC PRINTS; PR00700; PRTYPHTPASE.  
CC SMART; SM01194; PTPc; 1.  
CC PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
CC PROSITE; PS00036; TYR\_PHOSPHATASE\_2; 1.  
CC PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Cell division; Mitosis; Hydrolyase.  
FT ACT\_SITE 470 470 PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT SIMILARITY).  
SQ SEQUENCE 550 AA; 61587 MW; 5DB770AEAA59F03 CRC64;  
Query Match 2.7%; Score 11; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSCAGWGRTG 367  
DB 468 VHCSCAGWGRTG 478  
RESULT 19  
PTPE MOUSE STANDARD; PRT; 699 AA.  
ID AC P49456; Q62134; Q62444; Q64496;  
DT 01-FEB-1996 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-  
DE epsilon).  
GN PTPE OR PTPE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=FVB/N;  
RX MEDLINE=96064677; PubMed=7592814;  
RA Elson A., Leder P.;  
RT "Protein-tyrosine phosphatase epsilon. An isoform specifically  
RT expressed in mouse mammary tumors initiated by v-Ha-ras OR neu.";  
RL J. Biol. Chem. 270:26116-26122(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=DBA/2;  
RX STRAIN=FVB/N;  
RA Mukoyama Y.;  
RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6; TISSUE=Brain, and Lung;  
RA Hou E.W., Li S.L.;  
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 224-332 FROM N.A.  
RX STRAIN=BALB/c; TISSUE=Brain;  
RX MEDLINE=93086603; PubMed=1454056;  
RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;  
RT "Identification and typing of members of the protein-tyrosine  
RT phosphatase gene family expressed in mouse brain.";  
RL Mol. Biol. Rep. 16:241-248(1992).  
RN [5]  
RP SEQUENCE OF 224-332 FROM N.A.  
RX STRAIN=BALB/c; TISSUE=Brain;  
RX MEDLINE=95134232; PubMed=7832766;  
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;  
RT "A novel receptor-type protein tyrosine phosphatase with a single  
RT catalytic domain is specifically expressed in mouse brain.";  
RL Biochem. J. 305:499-504(1995).  
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
CC tyrosine + phosphate.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC  
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CC  
CC EMBL: U35368; AAC52281.1; -  
CC EMBL: D83484; EAA11927.1; -  
CC EMBL: U62387; AAB04553.1; -  
CC EMBL: Z23052; CAA80587.1; -  
CC EMBL: Z23053; CAA80588.1; -  
CC PIR: B61180; B61180.  
CC HSSP: P18052; 1YFO.

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DR MGD; MGI:97813; Ptpre.
DR InterPro; IPR000387; Tyr_phosphatase.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PTPPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 699 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT TRANSMEM 46 68 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 69 699 POTENTIAL.
FT DOMAIN 153 392 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 393 699 PROTEIN-TYROSINE PHOSPHATASE 1.
FT ACT_SITE 334 699 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 334 699 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT ACT_SITE 629 629 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 500 500 G -> A (IN REF. 2).
FT CONFLICT 506 506 G -> V (IN REF. 2).
FT CONFLICT 521 522 IV -> ML (IN REF. 2).
FT CONFLICT 606 606 M -> I (IN REF. 1).
FT SEQUENCE 699 AA; 80645 MW; 4D0467438017FEB CRC64;
Query Match 2.7%; Score 11; DB 1; Length 699;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 357 VHCSAGVGRG 367
Db 332 VHCSAGVGRG 342

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## RESULT 20

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ID _PTPE_HUMAN STANDARD; PRT; 700 AA.
AC P23469; Q96K06;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-epsilon).
GN PTPRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein tyrosine phosphatases.";
RT tyrosine phosphatases.";
RL EMBO J. 9:3241-3252(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=2118122; PubMed=12121439;
RA Wabakken T.K., Hauge H., Finne E.F., Wiedlocha A., Aasheim H.C.;
RT "Expression of human protein tyrosine phosphatase epsilon in leucocytes: a potential ERK pathway-regulating phosphatase.";
RL Scand. J. Immunol. 56:195-203(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); cytoplasmic (isoform 2).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=P23469-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P23469-2; Sequence=VSP_007778;
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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EMBL; X54134; CNA38069.1; --
EMBL; AJ315969; CAC86583.1; --
EMBL; BC050062; AAH50062.1; --
PIR; S12053; S12053.
HSP; P18052; IYFO.
Gene; HGNC:9669; PTPRE.
MIM; 60026; --
GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . . ; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
InterPro; IPR003595; PTPC motif.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR00700; PTPPHPTASE.
SMART; SM00194; PTPC; 2.
SMART; SM00404; PTPC_motif; 2.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal; Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 700 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT DOMAIN 20 46 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 47 69 POTENTIAL.
FT DOMAIN 70 700 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 154 393 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 394 700 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 335 335 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT ACT_SITE 630 630 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).

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RA Jones M., Stavrides G., Almeida J.P., Rabbage A.K., Bagnuley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Carter N.P.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clapp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobby V.B., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Howden P.J.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McCormack L.J., McMay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.R.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.,  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001)  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Long;  
 CC IsoId=P18433-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=P18433-2; Sequence=VSP\_005145;  
 CC Name=3;  
 CC IsoId=P18433-3; Sequence=VSP\_007776, VSP\_007777;  
 CC Name=4;  
 CC IsoId=P18433-4; Sequence=VSP\_007777;  
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC  
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 CC  
 CC EMBL; M34568; AAA36528.1; -;  
 CC EMBL; X54330; CAA38065.1; -;  
 CC EMBL; X54890; CAA38662.1; -;  
 CC EMBL; X53364; CAA37447.1; -;  
 CC EMBL; AL121905; CAC10336.1; -;  
 CC EMBL; AL121905; CAC10337.1; -;  
 CC PIR; A36065; A36065.  
 CC HSP; P18052; 1YPO.  
 CC Genew; HGNC:9664; PTPRA.  
 CC MIM; 176884; -;  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005001; P:transmembrane receptor protein tyrosine pho...; TAS.  
 CC InterPro; IPR003595; PTPC motif.  
 CC InterPro; IPR000387; TYR Phosphatase.  
 CC InterPro; IPR000242; Tyr\_PP.  
 CC Pfam; PF0102; Y\_phosphatase; 2.  
 CC PRINTS; PR00700; PTPRPHPTASE.  
 CC SMART; SM00194; PTPC; 2.  
 CC SMART; SM00404; PTPC motif; 2.  
 CC PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 CC PROSITE; PS00056; TYR PHOSPHATASE 2; 2.  
 CC PROSITE; PS00055; TYR PHOSPHATASE PTP; 2.  
 CC GlycoProtein; Transmembrane; Hydrolase; Phosphorylation; Signal;  
 KW Repeat; Alternative splicing.

FT SIGNAL 1 19  
 FT CHAIN 20 802  
 FT DOMAIN 20 142  
 FT TRANSMEM 143 185  
 FT DOMAIN 166 802  
 FT DOMAIN 241 500  
 FT DOMAIN 501 802  
 FT ACT\_SITE 442 442  
 FT ACT\_SITE 732 732  
 FT CARBOHYD 21 21  
 FT CARBOHYD 36 36  
 FT CARBOHYD 68 68  
 FT CARBOHYD 80 80  
 FT CARBOHYD 86 86  
 FT CARBOHYD 104 104  
 FT CARBOHYD 124 124  
 FT VARSPPLIC 139 147  
 FT VARSPPLIC 138 138  
 FT VARSPPLIC 179 187  
 FT CONFLICT 114 114  
 FT CONFLICT 122 122  
 FT CONFLICT 289 289  
 FT CONFLICT 367 367  
 FT CONFLICT 493 493  
 FT CONFLICT 786 786  
 SQ SEQUENCE 802 AA; 90599 MW; 8E964C3B56B5BE32 CRC64;  
 Query Match 2.7%; Score 11; DB 1; Length 802;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 357 VHCSAGVGRGTG 367  
 Db 440 VHCSAGVGRGTG 450  
 RESULT 24  
 PTRA\_MOUSE STANDARD; PRT; 829 AA.  
 ID AC P18052; Q61808;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase alpha precursor (BC 3.1.3.48) (R-BTP-  
 DE alpha) (LCA-related phosphatase).  
 GN PTPRA OR LRP OR PTPA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RC STRAIN=C57BL/6 X DBA/2;  
 RX MEDLINE=92080391; PubMed=2162042;  
 RA Matthews R.J., Cahir E.D., Thomas M.L.;  
 RT "Identification of an additional member of the protein-tyrosine-  
 RT phosphatase family: evidence for alternative splicing in the tyrosine  
 RT phosphatase domain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4444-4448(1990).  
 RN [2]  
 RP SEQUENCE OF 358-467 FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=95134322; PubMed=7832766;  
 RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;  
 RT "A novel receptor-type protein tyrosine phosphatase with a single  
 RT catalytic domain is specifically expressed in mouse brain.";  
 RL Biochem. J. 305:499-504(1995).  
 RN [3]



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CC CC EMBL; M14342; AAA39458.1; -  
 DR DR EMBL; M15344; AAA39461.1; -  
 DR DR EMBL; M15374; AAA40161.1; -  
 DR DR PIR; A23329; A23329.  
 DR DR PIR; A28334; A28334.  
 DR DR HSP; P18052; 1YPO.  
 DR DR MGD; MGI:97810; Ptpdc.  
 DR DR GO; GO:0005515; P:protein binding; IPI.  
 DR DR InterPro; IPR008957; FN III-like.  
 DR DR InterPro; IPR003961; FN III.  
 DR DR InterPro; IPR00387; TYR phosphatase.  
 DR DR InterPro; IPR00242; Tyr\_PP.  
 DR DR Pfam; PF00041; fn3; 3.  
 DR DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR DR PRINTS; PR00700; PRTYPHPTASE.  
 DR DR SMART; SM00060; FN3; 2.  
 DR DR SMART; SM00194; PTPC; 2.  
 DR DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 DR DR PROSITE; PS0056; TYR PHOSPHATASE 2; 2.  
 DR DR PROSITE; PS0055; TYR PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Antigen; T-cell; Repeat; Signal; Transmembrane;  
 KW Glycoprotein; Phosphorylation; Alternative splicing.  
 FT SIGNAL 1 23  
 FT CHAIN 24 1152 LEUCOCYTE COMMON ANTIGEN.  
 FT DOMAIN 24 425 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 426 447 POTENTIAL.  
 FT DOMAIN 448 1152 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 233 329 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 330 421 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 520 769 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FT DOMAIN 811 1084 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT ACT\_SITE 701 701 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT ACT\_SITE 1016 1016 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT ACT\_SITE 1016 1016 SIMILARITY).  
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGTG 367  
 DB 699 VHCSAGVGTG 709  
 RESULT 26  
 ID PTPO\_HUMAN STANDARD; PRT; 1216 AA.  
 AC Q16827; Q13101;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase O precursor (BC 3.1.3.48)  
 DE (Glomerular epithelial protein 1) (Protein tyrosine phosphatase U2)  
 DE (PTPase U2) (PTP-U2).  
 GN FTFPO OR GLEPPI FOR FTFU2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95273089; PubMed=7753550;  
 RA Seimiya H., Sawabe T., Inazawa J., Tsuruo T.;  
 RT "Cloning, expression and chromosomal localization of a novel gene for  
 RT protein tyrosine phosphatase (PTP-U2) induced by various  
 RT differentiation-inducing agents.";  
 RL Oncogene 10:1731-1738(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95394455; PubMed=7665166;  
 RA Wiggins R.C., Wiggins J.E., Goyal M., Wharram B.L., Thomas P.E.;  
 RT "Molecular cloning of cDNAs encoding human GLEPPI, a membrane protein  
 RT tyrosine phosphatase: characterization of the GLEPPI protein  
 RT distribution in human kidney and assignment of the GLEPPI gene to  
 RT human chromosome 12p12-p13.";  
 RL Genomics 27:174-181(1995).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Glomerulus of kidney. Also detected in brain,  
 CC lung and placenta.  
 CC -1- INDUCTION: By various differentiation-inducing agents.  
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
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 CC EMBL; Z48541; CAAB8425.1; -  
 CC EMBL; U20489; AAA82892.1; -  
 CC PIR; S60613; S60613.  
 CC HSP; P28827; IRPW.  
 CC Genew; HGNC:9678; PTERO.  
 CC MIM; 600579; -  
 CC GO; GO:0003687; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.  
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 CC InterPro; IPR008957; FN III-like.  
 CC InterPro; IPR003961; FN III.  
 CC InterPro; IPR00387; TYR phosphatase.  
 CC InterPro; IPR00242; Tyr\_PP.  
 CC Pfam; PF00041; fn3; 3.  
 CC Pfam; PF00102; Y\_phosphatase; 1.  
 CC PRINTS; PR00700; PRTYPHPTASE.  
 CC SMART; SM00060; FN3; 4.  
 CC SMART; SM00194; PTPC; 1.  
 CC PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE\_NEG.  
 CC PROSITE; PS0056; TYR PHOSPHATASE 2; 1.  
 CC PROSITE; PS0055; TYR PHOSPHATASE\_PTP; 1.  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 1216 RECEPTOR-TYPE PROTEIN-TYROSINE  
 FT PHOSPHATASE O.  
 FT DOMAIN 30 822 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 823 843 POTENTIAL.  
 FT DOMAIN 844 1216 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 50 124 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 142 211 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 245 306 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 327 399 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 434 508 FIBRONECTIN TYPE-III 5.

FT DOMAIN 528 608 FIBRONECTIN TYPE-III 6.  
 FT DOMAIN 630 703 FIBRONECTIN TYPE-III 7.  
 FT DOMAIN 723 793 FIBRONECTIN TYPE-III 8.  
 FT ACT\_SITE 938 1136 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 1136 1136 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 SIMILARITY).  
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 227 227 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 323 323 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 700 700 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 712 712 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 733 733 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 196 196 C -> S (IN REF. 2).  
 FT CONFLICT 205 205 V -> L (IN REF. 2).  
 FT CONFLICT 314 314 F -> V (IN REF. 2).  
 FT CONFLICT 441 441 F -> V (IN REF. 2).  
 FT CONFLICT 672 672 T -> A (IN REF. 2).  
 FT CONFLICT 698 698 I -> I (IN REF. 2).  
 FT CONFLICT 705 705 T -> A (IN REF. 2).  
 FT CONFLICT 753 753 K -> E (IN REF. 2).  
 FT CONFLICT 756 756 FQH -> CQQ (IN REF. 2).  
 FT CONFLICT 775 775 P -> S (IN REF. 2).  
 FT CONFLICT 790 790 S -> N (IN REF. 2).  
 FT CONFLICT 861 863 ANC -> VNF (IN REF. 2).  
 FT CONFLICT 876 903 MISSING (IN REF. 2).  
 SQ SEQUENCE 1216 AA; 138281 MW; D0A8A6027EF50203 CRC64;  
 Query Match 2.7%; Score 11; DB 1; Length 1216;  
 Best Local Similarity 100.0%; Pred. No. 0.0045;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGPLPET 241  
 DB 1007 YIATQGPLPET 1017  
 RESULT 27  
 CD45 RAT  
 ID CD45 RAT STANDARD; PRT; 1255 AA.  
 AC P04157;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Leukocyte common antigen variant 4 precursor (EC 3.1.3.48) (L-CA)  
 DE (CD45) (T200) (Fragment).  
 GN PTPRC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RA Barclay A.N., Jackson D.L., Willis A.C., Williams A.F.;  
 RA Submitted (MAY-1987) to the EMBL/GenBank/DBSJ databases.  
 [2]  
 RP SEQUENCE OF 190-1255 FROM N.A.  
 RX MEDLINE=85201691; PubMed=3158393;  
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;  
 RT "Evidence from cDNA clones that the rat leukocyte-common antigen of  
 RT (T200) spans the lipid bilayer and contains a cytoplasmic domain of  
 RT 80,000 Mr."  
 RL Cell 41:83-93(1985).  
 RN [3]

RP ALTERNATIVE SPLICING.  
 RX MEDLINE=87275817; PubMed=2440674;  
 RA Barclay A.N., Jackson D.L., Willis A.C., Williams A.F.;  
 RT "Lymphocyte specific heterogeneity in the rat leucocyte common  
 RT antigen (T200) is due to differences in polypeptide sequences near  
 RT the NH2-terminus."  
 RL EMBO J. 6:1259-1264(1987).  
 CC -!- FUNCTION: Required for T-cell activation through the antigen  
 CC receptor. The first PTPase domain has enzymatic activity, while  
 CC the second one seems to affect the substrate specificity of the  
 CC first one.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=P04157-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P04157-2; Sequence=VSP\_005167;  
 CC Name=3;  
 CC IsoId=P04157-3; Sequence=VSP\_005166;  
 CC Name=4;  
 CC IsoId=P04157-4; Sequence=VSP\_005165, VSP\_005168;  
 CC -!- TISSUE SPECIFICITY: Variants 4 and 3 are found in the lymph node,  
 CC variants 1 and 2 are found in thymocyte and lymph node.  
 CC -!- PTM: Heavily N- and O-glycosylated.  
 CC -!- PTM: The cytoplasmic domain contains potential phosphorylation  
 CC sites.  
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
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 CC or send an email to [licenses@isb-sib.ch](mailto:licenses@isb-sib.ch)).  
 DR EMBL; Y00065; CAA68272.1; -;  
 DR EMBL; Y00065; CAA68273.1; -;  
 DR EMBL; Y00065; CAA68274.1; -;  
 DR EMBL; Y00065; CAA68275.1; -;  
 DR EMBL; M25820; AAA41518.1; -;  
 DR EMBL; M25821; AAA41519.1; -;  
 DR EMBL; M25822; AAA41520.1; -;  
 DR EMBL; M25823; AAA41521.1; -;  
 DR HSSP; P18052; 1VFO.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF0102; Y\_phosphatase; 2.  
 DR PRINTS; PRD0700; PTPPHPTASE.  
 DR SMART; SM00194; ETPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Antigen; T-cell; Repeat; Signal; Transmembrane;  
 KW Glycoprotein; Phosphorylation; Alternative splicing.  
 FT NON TER 1 1  
 FT SIGNAL <1 5  
 FT CHAIN 6 1255 LEUKOCYTE COMMON ANTIGEN VARIANT 4.  
 FT DOMAIN 6 528 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 529 550 POTENTIAL.  
 FT DOMAIN 551 1255 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 341 432 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 433 524 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 623 872 PROTEIN-TYROSINE PHOSPHATASE 1.

FT DOMAIN 914 1187 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT ACT\_SITE 804 804 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 FT ACT\_SITE 1119 1119 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 12 53 Missing (in isoform 4).  
 FT VARSPLIC 12 102 Missing (in isoform 3).  
 FT VARSPLIC 53 143 Missing (in isoform 2).  
 FT VARSPLIC 103 143 Missing (in isoform 4).  
 FT CONFLICT 38 38 S -> R (IN REF. 3).  
 SQ SEQUENCE 1255 AA; 141208 MW; C257CBD2A355BCEA CRC64;

Query Match 2.7%; Score 11; DB 1; Length 1255;  
 Best Local Similarity 100.0%; Pred. No. 0.0047;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 357 VHCSAGVGTG 367  
 |||||  
 DB 802 VHCSAGVGTG 812

RESULT 28  
 PTP9 DROME STANDARD; PRT; 1301 AA.  
 AC P35832;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase 99A precursor (EC 3.1.3.48) (Receptor-  
 DE linked protein-tyrosine phosphatase 99A).  
 GN PTP99A.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID:7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RC TISSUE=Eye imaginal disk;  
 RX MEDLINE=92107930; PubMed=1662390;  
 RA Hariharan I.K., Chung P.-T., Rubin G.M.;  
 RT "Cloning and characterization of a receptor-class phosphotyrosine  
 RT phosphatase gene expressed on central nervous system axons in  
 RT Drosophila melanogaster.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11266-11270(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RC TISSUE=Embryo;  
 RX MEDLINE=92034989; PubMed=1657402;  
 RA Tian S.-S., Tsoulfas P., Zinn K.;  
 RT "Three receptor-linked protein-tyrosine phosphatases are selectively  
 RT expressed on central nervous system axons in the Drosophila embryo.";  
 RL Cell 67:675-685(1991).

RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Embryo;  
 RX MEDLINE=92034988; PubMed=1657401;  
 RA Yang X., Seow K.I., Bahri S.M., Oon S.H., Chia W.;  
 RT "Two Drosophila receptor-like tyrosine phosphatase genes are  
 RT expressed in a subset of developing axons and pioneer neurons in the  
 RT embryonic CNS.";  
 RL Cell 67:661-673(1991).  
 CC -!- FUNCTION: May play a key role in signal transduction and growth  
 CC control.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=P35832-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=P35832-2; Sequence=VSP 005142;  
 CC -!- TISSUE SPECIFICITY: Selectively expressed in a subset of axons and  
 CC pioneer neurons in the embryo.  
 CC -!- SIMILARITY: Contains 3 fibronectin type III domains.  
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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 CC -----  
 CC EMBL; M81795; AA28483.1; -;  
 CC EMBL; M80539; AA28485.1; -;  
 CC EMBL; M80464; AA28486.1; -;  
 CC PIR; A41622; A41622.  
 CC HSP; P18052; IYFO.  
 CC FlyBase; FBgn004369; Ptp99A.  
 CC GO; GO:0007415; P: defasciculation of motor neuron; IGI.  
 CC GO; GO:0008045; P: motor axon guidance; IGI.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003961; FN\_III.  
 CC InterPro; IPR00387; TVR phosphatase.  
 CC InterPro; IPR00242; Tyr\_PP.  
 CC Pfam; PF00041; fn3; 2.  
 CC Pfam; PF00102; Y\_phosphatase; 2.  
 CC PRINTS; PR00700; PTPPHPTASE.  
 CC SMART; SM00060; FN3; 2.  
 CC SMART; SM00194; PTP; 2.  
 CC PROSITE; PS00383; TVR\_PHOSPHATASE\_1; 1.  
 CC PROSITE; PS00056; TVR\_PHOSPHATASE\_2; 1.  
 CC PROSITE; PS50055; TVR\_PHOSPHATASE\_PTP; 2.  
 KW Transmembrane; Hydrolase; Repeat; Signal; Alternative splicing.  
 FT SIGNAL 1 29  
 FT CHAIN 30 1301 PROTEIN-TYROSINE PHOSPHATASE 99A.  
 FT DOMAIN 30 394 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 395 415 POTENTIAL.  
 FT DOMAIN 416 1301 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 64 168 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 169 268 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 269 368 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 497 747 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FT DOMAIN 748 975 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT ACT\_SITE 682 682 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 FT DOMAIN 1076 1091 POLY-GLN.  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).



KW Hydrolase; Antigen; T-cell; Repeat; Signal; Transmembrane;  
 KW Glycoprotein; Phosphorylation; Alternative splicing.

FT SIGNAL 1 23  
 FT CHAIN 24 1304  
 FT DOMAIN 24 575  
 FT TRANSMEM 576 597  
 FT DOMAIN 598 1304  
 FT DOMAIN 387 479  
 FT DOMAIN 480 571  
 FT DOMAIN 670 919  
 FT DOMAIN 961 1235  
 FT ACT\_SITE 851 851  
 FT ACT\_SITE 1167 1167  
 FT CARBOHYD 78 78  
 FT CARBOHYD 90 90  
 FT CARBOHYD 95 95  
 FT CARBOHYD 184 184  
 FT CARBOHYD 190 190  
 FT CARBOHYD 197 197  
 FT CARBOHYD 232 232  
 FT CARBOHYD 260 260  
 FT CARBOHYD 270 270  
 FT CARBOHYD 276 276  
 FT CARBOHYD 335 335  
 FT CARBOHYD 378 378  
 FT CARBOHYD 419 419  
 FT CARBOHYD 468 468  
 FT CARBOHYD 488 488  
 FT CARBOHYD 529 529  
 FT VARSPLIC 32 192  
 FT MUTAGEN 851 851  
 FT CONFLICT 650 650  
 FT CONFLICT 1207 1207  
 FT SEQUENCE 1304 AA; 147253 MW; A08FC22D6069BAF7 CRC64;

Query Match 2.7%; Score 11; DB 1; Length 1304;  
 Best Local Similarity 100.0%; Pred. No. 0.0048;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
 DB 849 VHCSAGVGRGTG 859

RESULT 30

PTPG CHICK  
 ID -PTPG-CHICK STANDARD; PRT; 1422 AA.  
 AC Q98936;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).  
 DE gamma).  
 GN Gallus gallus (Chicken).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Kidney;  
 RA Qinghua X., Xiaojun G., Cong S., Zong S.M., Jong Y.J., Chan J.,  
 RA Wang L.-H.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBSJ databases.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -1- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.

CC

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DR EMBL; U38349; AAB16910.1; -

DR PIR; T42636; T42636.

DR HSSP; P18052; 1YFO.

DR InterPro; IPR001148; Euk Coanhd.

DR InterPro; IPR008957; FN\_III-like.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR000387; TYR phosphatase.

DR Pfam; PF00194; carb anhydrase; 1.

DR Pfam; PF00041; fn3\_1.

DR Pfam; PF00102; Y\_phosphatase; 2.

DR PRINTS; PR00700; PRTIPHPTASE.

DR PRODOM; PD000865; Euk Coanhd; 1.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS00383; TYR PHOSPHATASE\_1; 1.

DR PROSITE; PS00056; TYR PHOSPHATASE\_2; 2.

DR PROSITE; PS00055; TYR PHOSPHATASE\_FTP; 2.

KW Glycoprotein; transmembrane; Hydrolase; Repeat; Signal.

FT SIGNAL 1 19

FT CHAIN 20 1422

FT DOMAIN 20 742

FT TRANSMEM 743 768

FT DOMAIN 769 1422

FT DOMAIN 56 322

FT DOMAIN 347 441

FT DOMAIN 846 1102

FT DOMAIN 1103 1422

FT ACT\_SITE 1037 1037

FT SITE 1328 1328

FT CARBOHYD 109 109

FT CARBOHYD 113 113

FT CARBOHYD 156 156

FT CARBOHYD 359 359

FT CARBOHYD 444 444

FT CARBOHYD 620 620

FT CARBOHYD 632 632

FT CARBOHYD 640 640

FT CARBOHYD 728 728

FT SEQUENCE 1422 AA; 159766 MW; DD484055993DA74F CRC64;

Query Match 2.7%; Score 11; DB 1; Length 1422;

Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367

DB 1035 VHCSAGVGRGTG 1045

RESULT 31

PTPB HUMAN

ID -PTPB HUMAN STANDARD; PRT; 1997 AA.

AC P23467;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Protein-tyrosine phosphatase beta precursor (EC 3.1.3.48) (R-PTP-beta).

DE beta).

GN PTPB OR PTPB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=9106016; PubMed=2170109;  
 RA Krueger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein  
 tyrosine phosphatases.";  
 RL EMO J. 9:3241-3252(1990).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC -1- SIMILARITY: Contains 16 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL: X54131; CAA38066.1; -  
 DR PIR: S12050; S12050.  
 DR HGSP: P18052; IYFO.  
 DR Genew: HGNC:9665; PTPRB.  
 DR MIM: 176882; -  
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO: GO:0005001; F:transmembrane receptor protein tyrosine pho. . ; TAS.  
 DR GO: GO:0006796; P:phosphate metabolism; TAS.  
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR000387; Tyr\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 14.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR GlycoProtein; Transmembrane; Hydrolase; Phosphorylation; Repeat;  
 KW Signal.  
 KW SIGNAL.  
 FT CHAIN 1 22  
 FT DOMAIN 23 1997  
 FT TRANSMEM 1622 1642  
 FT DOMAIN 1643 1997  
 FT DOMAIN 23 110  
 FT DOMAIN 111 200  
 FT DOMAIN 201 286  
 FT DOMAIN 287 374  
 FT DOMAIN 375 464  
 FT DOMAIN 465 551  
 FT DOMAIN 552 640  
 FT DOMAIN 641 728  
 FT DOMAIN 729 816  
 FT DOMAIN 817 904  
 FT DOMAIN 905 992  
 FT DOMAIN 993 1082  
 FT DOMAIN 1083 1170  
 FT DOMAIN 1171 1268  
 FT DOMAIN 1269 1352  
 FT DOMAIN 1353 1442  
 FT DOMAIN 1442 1597  
 FT ACT\_SITE 1504 1904  
 FT DOMAIN 28 28  
 FT DOMAIN 53 53  
 FT DOMAIN 75 75

FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 479 479 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 829 829 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1040 1040 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1096 1096 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1163 1163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1185 1185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1212 1212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1274 1274 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1367 1367 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1470 1470 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1474 1474 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1997 AA; 224267 MW; 691E99BA7A1515DD CRC64;  
 Query Match 2.7%; Score 11; DB 1; Length 1997;  
 Best Local Similarity 100.0%; Pred. No. 0.0074;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 357 VHCASGVGRG 367  
 Db 1902 VHCASGVGRG 1912  
 RESULT 32  
 LAR\_DROME STANDARD; PRT; 2029 AA.  
 ID LAR\_DROME  
 AC P16621;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase lar precursor (EC 3.1.3.48) (protein-  
 tyrosine-phosphate phosphohydrolase) (DLAR).  
 GN LAR.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=96178473; PubMed=8598047;  
 RA Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,  
 RA Saito H.;  
 RT "The transmembrane tyrosine phosphatase DLAR controls motor axon  
 guidance in Drosophila.";  
 RL Cell 94:611-622(1996).  
 CC -1- FUNCTION: It is possible that DLAR is a cell adhesion receptor.  
 CC It possesses an intrinsic protein tyrosine phosphatase activity  
 (PTPase). It controls motor axon guidance.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Selectively expressed in a subset of axons and  
 pioneer neurons in the embryo.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 9 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M27700; AAC28668.1; -  
CC EMBL; U36857; AAC47002.1; -  
CC EMBL; U36858; AAC47002.1; JOINED.  
CC EMBL; U36859; AAC47002.1; JOINED.  
CC EMBL; U36860; AAC47002.1; JOINED.  
CC EMBL; U36861; AAC47002.1; JOINED.  
CC EMBL; U36862; AAC47002.1; JOINED.  
CC EMBL; U36863; AAC47002.1; JOINED.  
CC EMBL; U36864; AAC47002.1; JOINED.  
CC EMBL; U36865; AAC47002.1; JOINED.  
CC EMBL; U36866; AAC47002.1; JOINED.  
CC PIR; A36182; TDFELK.  
CC HSP; P28827; IRPW.  
CC FlyBase; FBgn000464; Lar.  
CC GO; GO:004725; F:protein tyrosine phosphatase activity; IDA.  
CC GO; GO:003045; P:motor axon guidance; IMP.  
CC GO; GO:000470; P:protein amino acid dephosphorylation; IDA.  
CC InterPro; IPR008957; FN-III-like.  
CC InterPro; IPR003961; FN-III.  
CC InterPro; IPR003962; FN-III subd.  
CC InterPro; IPR007110; IG-1-like.  
CC InterPro; IPR003598; IG-2.  
CC InterPro; IPR000387; TYR phosphatase.  
CC InterPro; IPR000242; TYR\_PP.  
CC Pfam; PF00041; fn3; 9.  
CC Pfam; PF00047; ig3; 3.  
CC Pfam; PF00102; Y phosphatase; 2.  
CC PRINTS; PRO0014; ENTPPEIII.  
CC PRINTS; PRO0014; ENTPPEIII.  
CC PRINTS; PRO0700; PRTYPHPTASE.  
CC SMART; SM00050; FN3; 9.  
CC SMART; SM00408; IGC2; 3.  
CC SMART; SM00194; PTPC; 2.  
CC PROSITE; PS00835; IG-1-like; 3.  
CC PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
CC PROSITE; PS00566; TYR PHOSPHATASE 2; 2.  
CC PROSITE; PS00555; TYR PHOSPHATASE\_PTP; 2.  
CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
CC Cell adhesion; Immunoglobulin domain; Repeat.  
CC SIGNAL 1 32  
FT CHAIN 33 2029 PROTEIN-TYROSINE PHOSPHATASE LAR.  
FT DOMAIN 33 1377 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1378 1402 POTENTIAL.  
FT DOMAIN 1403 2029 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 36 128 IG-LIKE C2-TYPE 1.  
FT DOMAIN 140 224 IG-LIKE C2-TYPE 2.  
FT DOMAIN 234 316 IG-LIKE C2-TYPE 3.  
FT DOMAIN 320 417 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 418 512 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 513 607 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 608 706 FIBRONECTIN TYPE-III 4.  
FT DOMAIN 707 809 FIBRONECTIN TYPE-III 5.  
FT DOMAIN 810 906 FIBRONECTIN TYPE-III 6.  
FT DOMAIN 907 1007 FIBRONECTIN TYPE-III 7.  
FT DOMAIN 1008 1102 FIBRONECTIN TYPE-III 8.  
FT DOMAIN 1103 1207 FIBRONECTIN TYPE-III 9.  
FT DOMAIN 1208 1378 PROTEIN-TYROSINE PHOSPHATASE 1.  
FT DOMAIN 1379 1492 PROTEIN-TYROSINE PHOSPHATASE 2.  
FT DOMAIN 1493 1670 PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT ACT\_SITE 1671 1961 SIMILARITY).  
FT ACT\_SITE 1962 1961 PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT DISULFID 57 111 POTENTIAL).

FT DISULFID 161 209 POTENTIAL.  
FT DISULFID 256 301 POTENTIAL.  
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 553 553 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 666 666 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 721 721 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 774 774 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 915 915 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 962 962 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1183 1183 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1304 1304 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 2029 AA; 229027 MW; 536A0C794D3DC800 CRC64;  
  
Query Match 2.7%; Score 11; DB 1; Length 2029;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 357 VHCAGVGRGTG 367  
||| |||||  
DB 1668 VHCAGVGRGTG 1678  
  
RESULT 33  
LAR\_CASEL STANDARD; PRT; 2200 AA.  
AC Q9BMN8; Q09434; Q17859; Q20137; Q9BMN7;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Protein-tyrosine phosphatase Lar-like precursor (EC 3.1.3.48)  
DE (Protein-tyrosine-phosphate phosphohydrolase ptp-3).  
GN PTP-3 OR C09D8.1/C09D8.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.  
RC STRAIN=Bristol N2;  
RX MEDLINE=21956343; PubMed=11959824;  
RA Harrington R.J., Gutch M.J., Hengartner M.O., Tonks N.K.,  
RA Chisholm A.D.;  
RT "The C. elegans LAR-like receptor tyrosine phosphatase PTP-3 and the  
RT VAB-1 Eph receptor tyrosine kinase have partly redundant functions in  
RT morphogenesis.";  
RL Development 129:2141-2153(2002).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC STRAIN=Bristol N2;  
RA Coles L., Swinburne J.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP REVISIONS.  
RA Durbin R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Has a role in early neural and epidermal development;  
CC neuroblast movements during closure of the gastrulation cleft and  
CC epidermal morphogenesis. Vab-1 and ptp-3 may function redundantly  
CC within the same sets of neuronal precursors.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein; at adherens  
CC junctions.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=a; Synonyms=ptp-3a;  
CC IsoId=Q9BMN8-1; Sequence=Displayed;  
CC Name=b; Synonyms=ptp-3b;  
CC IsoId=Q9BMN8-2; Sequence=VSP 007007, VSP 007008;  
CC -!- TISSUE SPECIFICITY: Both isoforms are ubiquitously expressed in



FX MEDLINE=91006018; PubMed=2170109;  
RA Krueger N.X., Struuli M., Saito H.;  
RT "Structural diversity and evolution of human receptor-like protein  
RL tyrosine phosphatases.";  
RN EMBL J. 9:3241-3252(1990).  
[4]  
RP SEQUENCE OF 1749-1990 AND 2047-2280 FROM N.A. (ISOFORM LONG).  
RC TISSUE=Brain stem;  
RX MEDLINE=90384936; PubMed=2169617;  
RA Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M.,  
RT "Cloning of three human tyrosine phosphatases reveals a multigene  
RT family of receptor-linked protein-tyrosine-phosphatases expressed in  
RT brain.";  
RL Proc Natl Acad Sci U S A. 87:7000-7004(1990).  
CC -1- FUNCTION: May be involved in the regulation of specific  
CC developmental processes in the CNS.  
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -1- SUBUNIT: The carbonic-anhydrase like domain binds to contactin (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=P23471-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P23471-2; Sequence=VSP 005151;  
CC -1- TISSUE SPECIFICITY: Specifically expressed in the central nervous  
CC system, where it is localized in the Purkinje cell layer of the  
CC cerebellum, the dentate gyrus, and the subependymal layer of the  
CC anterior horn of the lateral ventricle. Developmentally regulated  
CC in the brain.  
CC -1- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
CC -1- CAUTION: Called RETPase beta in Ref.2 and Ref.4.  
CC  
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CC  
CC EMBL; M93426; AAA60225.1; -;  
CC EMBL; X54135; CAA38070.1; -;  
CC PIR; A46151; A46151.  
CC HSP; P18052; IYFO.  
CC GenBank; HGNC:9685; PTPRZ1.  
CC MIM; 176891; -;  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. . .; TAS.  
CC GO; GO:0007417; P:central nervous system development; TAS.  
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
CC InterPro; IPR001148; Euk\_Coanhd  
CC InterPro; IPR008957; FN\_III-like.  
CC InterPro; IPR003961; FN\_III.  
CC InterPro; IPR000387; TYR\_phosphatase.  
CC InterPro; IPR000242; Tyr\_PP.  
CC Pfam; PF00194; Carb\_anhydraz; 1.  
CC Pfam; PF00041; fn3; 1.  
CC Pfam; PF00102; Y\_phosphatase; 2.  
CC PRINTS; PR00700; PTPVPHPTASE.  
CC PRODOM; PD000865; Euk\_Coanhd; 1.  
CC SMART; SM00060; FN3; 1.  
CC SMART; SM00194; PTPC; 2.  
CC PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
CC PROSITE; PS00036; TYR\_PHOSPHATASE\_2; 2.  
CC PROSITE; PS00035; TYR\_PHOSPHATASE\_PTP; 2.  
CC Signal; Glycoprotein; Transmembrane; Hydrolase; Repeat;  
CC Alternative splicing.

FT SIGNAL 1 24  
FT CHAIN 25 2314  
FT  
FT DOMAIN 25 1635  
FT TRANSMEM 1636 1661  
FT DOMAIN 1662 2314  
FT DOMAIN 34 302  
FT DOMAIN 312 406  
FT DOMAIN 1744 1997  
FT DOMAIN 1998 2314  
FT ACT\_SITE 1932 1932  
FT  
FT SITE 2222 2222  
FT CARBOHYD 105 105  
FT CARBOHYD 134 134  
FT CARBOHYD 223 223  
FT CARBOHYD 232 232  
FT CARBOHYD 324 324  
FT CARBOHYD 381 381  
FT CARBOHYD 497 497  
FT CARBOHYD 501 501  
FT CARBOHYD 552 552  
FT CARBOHYD 587 587  
FT  
FT CARBOHYD 602 602  
FT CARBOHYD 629 629  
FT CARBOHYD 637 637  
FT  
FT CARBOHYD 677 677  
FT CARBOHYD 997 997  
FT  
FT CARBOHYD 1017 1017  
FT CARBOHYD 1050 1050  
FT CARBOHYD 1082 1082  
FT CARBOHYD 1122 1122  
FT CARBOHYD 1456 1456  
FT CARBOHYD 1548 1548  
FT  
FT CARBOHYD 1550 1550  
FT  
FT CARBOHYD 1561 1561  
FT CARBOHYD 1617 1617  
FT VARSPLIC 755 1614  
FT  
FT CONFLICT 1722 1728  
FT SEQUENCE 2314 AA; 254528 MW; 77DBEFA40F5FB42 CRC64;  
Query Match 2.7%; Score 11; DB 1; Length 2314;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 357 VHCSAGVGRTG 367  
||| ||||| |||||  
Db 1930 VHCSAGVGRTG 1940  
  
RESULT 35  
PTPZ RAT STANDARD; PRT; 2316 AA.  
ID PTPZ RAT  
AC Q62656; Q62621;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase zeta precursor  
DE (RC 3.1.3.48) (R-PTP-zeta) (Phosphacan) (3F8 chondroitin sulfate  
DE proteoglycan) (3H1 keratan sulfate proteoglycan).  
DE PIPRZ1 OR PIPRZ2 OR PTPZ.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=96063026; PubMed=7579599;  
 RA Maurel P., Meyer-Puttlitz B., Flad M., Margolis R.U.,  
 RA Margolis R.K.,  
 RT "Nucleotide sequence and molecular variants of rat receptor-type  
 RT protein tyrosine phosphatase-zeta/beta.";  
 RL DNA Seq. 5:323-328 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=94195772; PubMed=7511813;  
 RA Maurel P., Rauch U., Flad M., Margolis R.K., Margolis R.U.,  
 RA Margolis R.K., Grumet M., Margolis R.U.,  
 RT "Phosphacan, a chondroitin sulfate proteoglycan of brain that  
 RT interacts with neurons and neural cell-adhesion molecules, is an  
 RT extracellular variant of a receptor-type protein tyrosine  
 RT phosphatase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2512-2516 (1994).  
 RN [3]  
 RP BINDING TO N-CAM AND NG-CAM (PHOSPHACAN).  
 RC MEDLINE=95096181; PubMed=7528221;  
 RX Milev P., Friedlander D.R., Sakurai T., Karthikeyan L., Flad M.,  
 RA Margolis R.K., Grumet M., Margolis R.U.,  
 RA "Interactions of the chondroitin sulfate proteoglycan phosphacan, the  
 RT extracellular domain of a receptor-type protein tyrosine phosphatase,  
 RT with neurons, glia, and neural cell adhesion molecules.";  
 RL J. Cell Biol. 127:1703-1715 (1994).  
 RN [4]  
 RP BINDING TO TENASCIN (PHOSPHACAN).  
 RC MEDLINE=94215329; PubMed=7512950;  
 RX Grumet M., Milev P., Sakurai T., Karthikeyan L., Bourdon M.,  
 RA Margolis R.K., Margolis R.U.,  
 RA "Interactions with tenascin and differential effects on cell adhesion  
 RT of neurocan and phosphacan, two major chondroitin sulfate  
 RT proteoglycans of nervous tissue.";  
 RL J. Biol. Chem. 269:12142-12146 (1994).  
 RN [5]  
 RP INTERACTION WITH CONTACTIN.  
 RC MEDLINE=95354206; PubMed=7628014;  
 RX Peles E., Nativ M., Campbell P.L., Sakurai T., Martinez R., Lev S.,  
 RA Clary D.O., Schilling J., Barnea G., Plowman G.D., Grumet M.,  
 RA Schlesinger J.,  
 RT "The carbonic anhydrase domain of receptor tyrosine phosphatase beta  
 RT is a functional ligand for the axonal cell recognition molecule  
 RT contactin.";  
 RL Cell 82:251-260 (1995).  
 CC -1- FUNCTION: May be involved in the regulation of specific  
 CC developmental processes in the CNS.  
 CC -1- FUNCTION: Phosphacan, previously designated 3F8 chondroitin  
 CC sulfate proteoglycan or 3H1 keratan sulfate proteoglycan depending  
 CC on the glycosylation status, is a soluble nervous tissue-specific  
 CC proteoglycan. It is synthesized by glia and binds to neurons and  
 CC to the neural cell adhesion molecules tenascin, N-CAM or NG-CAM  
 CC but not to laminin and fibronectin. Phosphacan acts as a potent  
 CC inhibitor of cell adhesion and neurite outgrowth.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBUNIT: The carbonic-anhydrase like domain binds to contactin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=Long;  
 CC IsoId=Q62656-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=Q62656-2; Sequence=VSP\_005152;  
 CC Name=3; Synonyms=Phosphacan;  
 CC IsoId=Q62656-3; Sequence=VSP\_005153, VSP\_005154;  
 CC TISSUE SPECIFICITY: Nervous tissue specific.  
 CC -1- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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 -----  
 DR EMBL; U09357; AAC52207.1; -;  
 DR EMBL; U04998; AAC52383.1; -;  
 DR HSSP; P18052; LYFO.  
 DR InterPro; IPR001148; Euk\_COahnd.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR000387; TYR\_Phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00194; carb\_anhydase; 1.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRYTPHPTASE.  
 DR ProDom; PD000865; Euk\_COahnd; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE PTP; 2.  
 KW Signal; Glycoprotein; Transmembrane; Hydrolase; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 24  
 FT CHAIN 25 2316 RECEPTOR-TYPE PROTEIN-TYROSINE  
 FT DOMAIN 25 1637 PHOSPHATASE ZETA  
 FT TRANSMEM 1638 1663 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1664 2316 POTENTIAL.  
 FT DOMAIN 34 302 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 312 406 CARBONIC-ANHYDRASE LIKE.  
 FT DOMAIN 1746 1999 FIBRONECTIN TYPE-III.  
 FT DOMAIN 2000 2316 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FT DOMAIN 951 954 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT DOMAIN 1225 1230 POLY-SER.  
 FT DOMAIN 1426 1439 POLY-SER.  
 FT ACT SITE 1934 1934 POLY-ASP.  
 FT SITE 2224 2224 ANCESTRAL ACTIVE SITE.  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 497 497 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 595 595 O-LINKED (XYL. . .) (CHONDROITIN SULFATE  
 FT (POTENTIAL).  
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 645 645 O-LINKED (XYL. . .) (CHONDROITIN SULFATE  
 FT (POTENTIAL).  
 FT CARBOHYD 685 685 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 786 786 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1005 1005 O-LINKED (XYL. . .) (CHONDROITIN SULFATE  
 FT (POTENTIAL).  
 FT CARBOHYD 1025 1025 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1058 1058 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1463 1463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1550 1550 O-LINKED (XYL. . .) (CHONDROITIN SULFATE  
 FT (POTENTIAL).  
 FT CARBOHYD 1552 1552 O-LINKED (XYL. . .) (CHONDROITIN SULFATE  
 FT (POTENTIAL).  
 FT CARBOHYD 1563 1563 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1611 1611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1619 1619 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 763 1615 Missing (in isoform 2).  
 FT VARSPLIC 1616 1616 /FTID=VSP\_005152.  
 FT VARSPLIC 1616 1616 R -> G (in isoform 3).  
 FT /FTID=VSP\_005153.

FT VARSELIC 1617 2316 Missing (in isoform 3).  
 FT /FTIG=VSP 005154.  
 SQ SEQUENCE 2316 AA; 255340 MW; 419EA9B9BDD165F CRC64;

Query Match 2.7%; Score 11; DB 1; Length 2316;  
 Best Local Similarity 100.0%; Pred. No. 0.0085;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367  
 Db 1932 VHCAGVGRTG 1942

## RESULT 36

PTNI\_HUMAN STANDARD; PRT; 458 AA.  
 AC Q9952;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)  
 DE (Brain-derived phosphatase).  
 GN PTPN18 OR BDPI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.  
 RX MEDLINE=97108674; PubMed=8950995;  
 RA Kim Y.W., Wang H.Y., Sures I., Lammers R., Martell K.J., Ullrich A.;  
 RT "Characterization of the PEST family protein tyrosine phosphatase  
 BDPI.";  
 RL Oncogene 13:2275-2279(1996).  
 CC -!- FUNCTION: Differentially dephosphorylate autophosphorylated  
 CC tyrosine kinases which are known to be overexpressed in tumor  
 CC tissues.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -!- TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-  
 CC derived cell lines.  
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

EMBL; X79568; CAA56105.1; --  
 HSP; Q66124; ZSHP.  
 DR Genew; HGNC:9649; PTPN18.  
 DR MIM; 606587; --  
 DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phosphatase.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.  
 FT DOMAIN 26 291 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 229 229 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 458 AA; 50384 MW; 46BCALE17C278B1 CRC64;

Query Match 2.2%; Score 9; DB 1; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 YIATQGPLP 239  
 Db 101 YIATQGPLP 109

## RESULT 37

PTP2\_YEAST STANDARD; PRT; 750 AA.  
 AC P29461;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase 2 (EC 3.1.3.48) (PTPase 2).  
 GN PTP2 OR YOR208W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92250559; PubMed=1577774;  
 RA Guan K., Deschenes R.J., Dixon J.E.;  
 RT "Isolation and characterization of a second protein tyrosine  
 RT phosphatase gene, PTP2, from Saccharomyces cerevisiae.";  
 RL J. Biol. Chem. 267:10024-10030(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92196117; PubMed=1549598;  
 RA Ota I.M., Varshavsky A.;  
 RT "A gene encoding a putative tyrosine phosphatase suppresses lethality  
 RT of an N-end rule-dependent mutant.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2355-2359(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA James P., Hall B.D., Whelen S., Craig E.A.;  
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.

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 -----

EMBL; M85287; -- NOT ANNOTATED\_CDS.  
 DR EMBL; M82872; AAA34922.1; --  
 DR EMBL; M38723; AAB59323.1; --  
 DR EMBL; Z75116; CAA99423.1; --  
 DR PIR; S67100; S67100.  
 DR HSSP; P18052; LYFO.  
 DR GERMOnline; 143796; --  
 DR SGD; S0005734; PTP2.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.

DR PRINTS: PR00700; PRTYPHPTASS.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.  
 FT ACT\_SITE 666 666 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT ACT\_SITE 666 666 SIMILARITY).  
 FT CONFLICT 371 371 L -> S (IN REF. 3).  
 FT CONFLICT 474 475 KL -> NV (IN REF. 1).  
 FT CONFLICT 660 661 SP -> GA (IN REF. 3).  
 SQ SEQUENCE 750 AA; 85968 MM; 1033DD2F0AA23BD35 CRC64;  
 Query Match 2.2%; Score 9; DB 1; Length 750;  
 Best Local Similarity 100.0%; Pred. No. 0.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 354 PLLVHCASG 362  
 Db 661 PLLVHCASG 669  
 RESULT 38  
 PTN3 HUMAN  
 ID PTN3 HUMAN STANDARD; PRT; 913 AA.  
 AC P26045;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase H1) (PTP-H1).  
 GN PTPN3 OR PTPH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RX MEDLINE=91296738; PubMed=1648725;  
 RA Yang Q., Tonks N.K.;  
 RT "Isolation of a cDNA clone encoding a human protein-tyrosine  
 RT phosphatase with homology to the cytoskeletal-associated proteins  
 RT band 4.1, ezrin, and talin".  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).  
 [2]  
 RP SEQUENCE OF 194-896 FROM N.A.  
 RC TISSUE=Colon;  
 RX MEDLINE=92327504; PubMed=1626183;  
 RA Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,  
 RA Imai K., Yachi A.;  
 RT "cDNA cloning of new protein tyrosine phosphatases in the human  
 RT colon".  
 RL Tumour Biol. 13:180-186(1992).  
 [3]  
 RP SEQUENCE OF 899-913 FROM N.A.  
 RX MEDLINE=95179278; PubMed=7874267;  
 RA Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,  
 RA Yachi A.;  
 RT "Expression of cytoskeletal-associated protein tyrosine phosphatase  
 RT PTPH1 mRNA in human hepatocellular carcinoma".  
 RL J. Gastroenterol. 29:727-732(1994).  
 CC -1- FUNCTION: May act at junctions between the membrane and the  
 CC cytoskeleton.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC -1- SIMILARITY: Contains 1 FERM domain.  
 CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M64572; AAA35647.1; -;  
 CC EMBL; S19392; AAB22439.2; -;  
 CC EMBL; S76309; AAB33583.1; -;  
 CC PIR; A41109; A41109.  
 CC HSSP; F18031; 1FTY.  
 CC Genew; HGNC:9655; PTPN3.  
 CC MIM; 176877; -;  
 CC GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.  
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 CC InterPro; IPR000299; Band\_4.1.  
 CC InterPro; IPR001478; PDZ\_1.  
 CC InterPro; IPR000387; TYR\_phosphatase.  
 CC InterPro; IPR000242; Tyr\_PP.  
 CC Pfam; PF00373; Band\_41; 1.  
 CC Pfam; PF00595; PDZ; 1.  
 CC Pfam; PF00102; Y\_phosphatase; 1.  
 CC PRINTS; PR00935; BAND41.  
 CC SMART; SM00295; B41; 1.  
 CC SMART; SM00228; PDZ; 1.  
 CC SMART; SM00194; PTPC; 1.  
 CC PROSITE; PS00660; FERM\_1; 1.  
 CC PROSITE; PS00661; FERM\_2; 1.  
 CC PROSITE; PS00557; FERM\_3; 1.  
 CC PROSITE; PS00106; PDZ; 1.  
 CC PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 CC PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
 CC PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Structural protein; Cytoskeleton; Hydrolase.  
 FT DOMAIN 29 312  
 FT DOMAIN 510 582  
 FT DOMAIN 670 913  
 FT ACT\_SITE 842 842  
 FT ACT\_SITE 842 842  
 SQ SEQUENCE 913 AA; 104029 MW; 29A539ACDE2F1515 CRC64;  
 Query Match 2.2%; Score 9; DB 1; Length 913;  
 Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGPLP 239  
 Db 714 YIATQGPLP 722  
 RESULT 39  
 PTPX\_MOUSE  
 ID PTPX\_MOUSE STANDARD; PRT; 1001 AA.  
 AC P80560; O09134; P70328;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)  
 DE (R-PTP-N2) (PTP IA-2beta) (Protein tyrosine phosphatase-NP) (PTP-NP).  
 GN PTPN2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICE; TISSUE=Brain;  
 RX MEDLINE=96281667; PubMed=8681804;  
 RA Chiang M.-K., Flanagan J.G.;  
 RT "PTP-NP, a new member of the receptor protein tyrosine phosphatase  
 RT family, implicated in development of nervous system and pancreatic  
 RT endocrine cells".





PT ACT\_SITE 934 934 PHOSPHOCYSTEINE INTERMEDIATE (POTENTIAL).  
 FT SITE 415 416 CLEAVAGE SITE (BY SIMILARITY).  
 FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1004 AA; 111863 MW; A733929811B486FB2 CRC64;  
 Query Match 2.2%; Score 9; DB 1; Length 1004;  
 Best Local Similarity 100.0%; Pred. No. 0.53; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGPLP 239  
 DB 805 YIATQGPLP 813  
 RESULT 41  
 ID PTFX MACNE STANDARD; PRT; 1013 AA.  
 AC 002695;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)  
 DE (R-PTP-N2) (M1853).  
 GN PTPRN2.  
 OS Macaca nemestrina (pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancratic islets;  
 RX MEDLINE=97254813; PubMed=9100223;  
 RA Lagasse J., Jelinek L., Sexson S., Lofton-Day C.E., Breininger J.,  
 Sheppard P., Jelinek W., Hagopian W.A.;  
 RT "An islet-cell protein tyrosine phosphatase is a likely precursor to  
 the 37-kDa autoantigen in type 1 diabetes: human and macaque  
 sequences, tissue distribution, unique and shared epitopes, and  
 predictive autoantibodies";  
 RT Mol. Med. 3:163-173(1997).  
 RL  
 CC -!- FUNCTION: Implicated in development of nervous system and  
 pancreatic endocrine cells.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: Brain, prostate, pancreatic islets. Lower  
 expression in spinal cord, thyroid, adrenal medulla and  
 gastrointestinal tract.  
 CC -!- PTM: Appears to undergo multiple proteolytic cleavage at  
 consecutive basic residues (by similarity).  
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U91574; AAC51186.1; ..  
 DR HSP; P18052; 1YFO.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR00242; Tyr\_Pp.  
 DR Pfam; PF0102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE ptp; 1.  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 1013 RECEPTOR-TYPE PROTEIN-TYROSINE

FT DOMAIN 20 613 PHOSPHATASE N2.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 614 634 POTENTIAL.  
 FT DOMAIN 635 1013 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 768 1002 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 943 943 PHOSPHOCYSTEINE INTERMEDIATE (POTENTIAL).  
 FT SITE 426 562 CLEAVAGE SITE (BY SIMILARITY).  
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1013 AA; 111190 MW; 4808D43937A2EF59 CRC64;  
 Query Match 2.2%; Score 9; DB 1; Length 1013;  
 Best Local Similarity 100.0%; Pred. No. 0.54; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGPLP 239  
 DB 814 YIATQGPLP 822  
 RESULT 42  
 ID PTFX HUMAN STANDARD; PRT; 1015 AA.  
 AC Q92932; Q8N4I5; Q92662;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)  
 DE (R-PTP-N2) (Islet cell autoantigen related protein) (ICAAAR) (IAR)  
 DE (Phogrin).  
 GN PTPRN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=97032784; PubMed=8878534;  
 RA Kawasaki E., Hutton J.C., Eisenbarth G.S.;  
 RT "Molecular cloning and characterization of the human transmembrane  
 protein tyrosine phosphatase homologue, phogrin, an autoantigen of  
 type 1 diabetes";  
 RT Biochem. Biophys. Res. Commun. 227:440-447(1996).  
 RL  
 CC -!- FUNCTION: Phogrin is a member of the human transmembrane  
 protein tyrosine phosphatase homologue, phogrin, an autoantigen of  
 type 1 diabetes.  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: Brain, prostate, pancreatic islets. Lower  
 expression in spinal cord, thyroid, adrenal medulla and  
 gastrointestinal tract.  
 CC -!- PTM: Appears to undergo multiple proteolytic cleavage at  
 consecutive basic residues (by similarity).  
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U91574; AAC51186.1; ..  
 DR HSP; P18052; 1YFO.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR00242; Tyr\_Pp.  
 DR Pfam; PF0102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE ptp; 1.  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 1013 RECEPTOR-TYPE PROTEIN-TYROSINE

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton Z., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.B.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Implicated in development of nervous system and  
pancreatic endocrine cells.  
CC -!- CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q92932-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q92932-2; Sequence=VSP\_007779;  
CC Notes=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Highest levels in brain and pancreas. Lower  
levels in trachea, prostate, stomach and spinal chord.  
CC -!- DOMAIN: The cytoplasmic domain appears to contain the  
autocatalytic epitopes.  
CC -!- PTM: Appears to undergo multiple proteolytic cleavage at  
consecutive basic residues.  
CC -!- DISEASE: Autoantigen in insulin-dependent diabetes mellitus  
(IDDM).  
CC -!- MISCELLANEOUS: Optimum activity is measured at pH 4.5.  
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
CC  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL: U66702; AAC50742.1; -;  
CC EMBL: Y08569; CAA69880.1; -;  
CC EMBL: AF07555; AAB63600.1; -;  
CC EMBL: BC034040; AAB34040.1; -;  
CC F01; JCS062; JCS062;  
CC F01; JCS263; JCS263;  
CC HSP; P18052; IYFO.  
CC Genes: HGNC:9677; PTPRN2.  
CC MIM: 601698; -;  
CC GO: GO:0005887; C: integral to plasma membrane; TAS.  
CC GO: GO:0005001; P: transmembrane receptor protein tyrosine pho. . .; TAS.  
CC GO: GO:0006470; P: protein amino acid dephosphorylation; TAS.  
CC InterPro: IPR003595; PTPC\_motif.  
CC InterPro: IPR000387; TYR\_phosphatase.  
CC InterPro: IPR000242; TYR\_PP.  
CC Pfam: PF00102; Y\_phosphatase; 1.  
CC PRINTS: PR00700; PRTVPHPTASE.  
CC SMART: SM00194; PTPC; 1.  
CC SMART: SM00404; PTPC\_motif; 1.  
CC PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
CC PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
CC PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
KW Diabetes mellitus; Alternative splicing.  
CC SIGNAL 1 21 POTENTIAL.  
CC RECEPTOR-TYPE PROTEIN-TYROSINE  
CC PHOSPHATASE N2.  
CC DOMAIN 22 615  
CC EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 616 636  
CC POTENTIAL.  
CC DOMAIN 637 1015  
CC CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 770 1004  
CC PROTEIN-TYROSINE PHOSPHATASE.

FT ACT\_SITE 945 945 PHOSPHOCYSTEINE INTERMEDIATE (BY  
FT SITE 427 428 CLEAVAGE SITE (POTENTIAL).  
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 519 547 Missing (in isoform 2).  
FT /FTID=VSP\_007779.  
FT MUTAGEN 945 945 C->S: LOSS OF ACTIVITY.  
FT CONFLICT 208 208 P -> S (IN REF. 2 AND 3).  
FT CONFLICT 247 247 S -> G (IN REF. 2).  
FT CONFLICT 323 323 G -> R (IN REF. 2).  
FT CONFLICT 325 325 S -> N (IN REF. 2).  
SQ SEQUENCE 1015 AA; 111281 MW; 82AC3CC9F59A6C97 CRC64;  
Query Match 2-2%; Score 9; DB 1; Length 1015;  
Best Local Similarity 100.0%; Pred. No. 0.54; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;  
QY 231 YIATQGPLP 239  
DB 816 YIATQGPLP 824  
RESULT 43  
PTPL DROME  
ID PTPL DROME STANDARD; PRT: 1631 AA.  
AC P35992;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Protein-tyrosine phosphatase 10D precursor (EC 3.1.3.48) (Receptor-  
DE linked protein-tyrosine phosphatase 10D).  
GN PTP10D.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Phylloidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RP TISSUE=Embryo;  
RX MEDLINE=92034989; PubMed=1657402;  
RA Tian S.-S., Tsoulfas P., Zinn K.;  
RT "Three receptor-linked protein-tyrosine phosphatases are selectively  
expressed on central nervous system axons in the Drosophila embryo.";  
RL Cell 67:675-685(1991).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RP TISSUE=Embryo;  
RX MEDLINE=92034988; PubMed=1657401;  
RA Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W.;  
RT "Two Drosophila receptor-like tyrosine phosphatase genes are  
expressed in a subset of developing axons and pioneer neurons in the  
embryonic CNS.";  
RL Cell 67:661-673(1991).  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=P35992-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P35992-2; Sequence=VSP\_005143, VSP\_005144;  
CC -!- TISSUE SPECIFICITY: Selectively expressed in a subset of axons and  
pioneer neurons in the embryo.  
CC -!- SIMILARITY: Contains 12 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
CC  
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CC



CL14\_MOUSE  
ID CL14\_MOUSE STANDARD; PRT; 573 AA.  
AC FL9467;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cell surface antigen 114/A10 precursor (lymphocyte antigen 64).  
GN LY64.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89197960; PubMed=2784793;  
RA Dougherty G.J., Kay R.J., Humphries R.K.;  
RT "Molecular cloning of 114/A10, a cell surface antigen containing  
RT highly conserved repeated elements, which is expressed by murine  
RT hemopoietic progenitor cells and interleukin-3-dependent cell  
RT lines.";  
RL J. Biol. Chem. 264:6509-6514 (1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loqueirano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: May have a positive regulatory role in the cellular  
CC response to IL-3.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PTM: THE SER/THR-RICH TANDEM REPEATS MAY SERVE AS SITES OF  
CC EXTENSIVE GLYCOSYLATION  
CC -!- PTM: THE MOTIF SER-GLY CONSERVED IN ALL 8 SER/THR-RICH REPEATS MAY  
CC SERVE AS THE SITE OF ATTACHMENT OF GLYCOSAMINOGLYCAN SIDE CHAINS.  
CC -!- SIMILARITY: Contains 3 EGF-like domains.  
CC -!- SIMILARITY: Contains 1 SEA domain.  
CC  
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CC  
CC ENBL; J04634; AAA37239.1; --  
DR ENBL; BC024321; AAH24321.1; --  
DR PIR; A35533; A35533.  
DR MGD; MGI:103190; Ly64.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000082; SEA\_domain.  
DR Pfam; PF00008; EGF; 1.  
DR SMART; SM00181; EGF; 1.  
DR

DR SMART; SM00200; SEA; 1.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS00024; SEA; 1.  
KW Glycoprotein; Signal; Antigen; EGF-like domain; Repeat; Transmembrane.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 573 CELL SURFACE ANTIGEN 114/A10.  
FT DOMAIN 18 480 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 481 508 POTENTIAL.  
FT DOMAIN 509 573 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 17 230 8 X TANDEM REPEATS, SER/THR-RICH.  
FT REPEAT 17 43 1.  
FT REPEAT 44 70 2.  
FT REPEAT 71 97 3.  
FT REPEAT 98 124 4.  
FT REPEAT 125 151 5.  
FT REPEAT 152 178 6.  
FT REPEAT 179 205 7 (NEAR PERFECT).  
FT REPEAT 206 230 8 (APPROXIMATE).  
FT DOMAIN 233 273 EGF-LIKE 1.  
FT DOMAIN 274 384 SEA.  
FT DOMAIN 385 425 EGF-LIKE 2.  
FT DOMAIN 425 467 EGF-LIKE 3.  
FT DISULFID 237 248 BY SIMILARITY.  
FT DISULFID 242 257 BY SIMILARITY.  
FT DISULFID 259 272 BY SIMILARITY.  
FT DISULFID 369 402 BY SIMILARITY.  
FT DISULFID 394 408 BY SIMILARITY.  
FT DISULFID 410 424 BY SIMILARITY.  
FT DISULFID 429 441 BY SIMILARITY.  
FT DISULFID 433 451 BY SIMILARITY.  
FT DISULFID 453 466 BY SIMILARITY.  
FT CARBOHYD 266 286 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 573 AA; 58701 MW; 1154C4F04E2D58A9 CRC64;  
Query Match 2.0%; Score 8; DB 1; Length 573;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 SARSAMRD 152  
| | | | |  
Db 335 SARSAMRD 342  
RESULT 46  
PTN8\_MOUSE STANDARD; PRT; 802 AA.  
AC P29352;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)  
DE (Hematopoietic cell protein-tyrosine phosphatase 702-PEP).  
GN PTPN8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92236615; PubMed=1373816;  
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;  
RT "Characterization of hematopoietic intracellular protein tyrosine  
RT phosphatases: description of a phosphatase containing an SH2 domain  
RT and another enriched in proline-, glutamic acid-, serine-, and  
RT threonine-rich sequences.";  
RL Mol. Cell. Biol. 12:2396-2405 (1992).  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.



OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hermel J.-M., Dirckx R., Solimena M.;  
 RT "Biochemical analysis of the IDDM autoantigen ICA512.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.  
 RA MEDLINE=99388259; PubMed=10457160;  
 RM Hermel J.-M., Dirckx R., Solimena M.;  
 RT "Post-translational modifications of ICA512, a receptor tyrosine  
 phosphatase-like protein of secretory granules.";  
 RL Eur. J. Neurosci. 11:2609-2620(1999).  
 CC [1] FUNCTION: Implicated in neuroendocrine secretory processes. May be  
 involved in processes specific for neurosecretory granules, such  
 as their biogenesis, trafficking or regulated exocytosis or may  
 have a general role in neuroendocrine functions. Lacks intrinsic  
 enzyme activity. May play a role in the regulation of secretory  
 granules via its interaction with SNTB2 (By similarity).  
 CC [2] SUBUNIT: Interacts with phosphorylated SNTB2, protecting it from  
 protein cleavage by CAPN1. Dephosphorylation of SNTB2 upon insulin  
 stimulation disrupts the interaction and results in its cleavage  
 (By similarity).  
 CC [3] SUBCELLULAR LOCATION: Type I membrane protein. Neuroendocrine  
 secretory granules.  
 CC [4] PTM: N-glycosylated.  
 CC [5] SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
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 CC EMBL; AF075170; AAD41665.1; -  
 DR HSP; Q06124; 2SHP.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_Pp.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRYPERPHASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 DR PROSITE; PS00556; TYR\_PHOSPHATASE 2; 1.  
 DR PROSITE; PS00555; TYR\_PHOSPHATASE\_Ptp; 1.  
 KW Receptor; Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 34  
 FT CHAIN 35 979 PROTEIN-TYROSINE PHOSPHATASE-LIKE N.  
 FT DOMAIN 35 575 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 576 600 POTENTIAL.  
 FT DOMAIN 601 979 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 696 979 PROTEIN-TYROSINE PHOSPHATASE-LIKE.  
 FT ACT\_SITE 909 909 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 SIMILARITY).  
 FT SITE 448 449 CLEAVAGE SITE.  
 FT CARBOHYD 506 506 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 524 524 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 979 AA; 105908 MW; 288DA2DBE780CB67 CRC64;  
 Query Match 2.0%; Score 8; DB 1; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 6.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 VIATQGPL 238  
 DB 780 VIATQGPL 787  
 RESULT 49  
 ID PTEN\_HUMAN STANDARD; PRT; 979 AA.

AC 015849; C08319;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase-like N precursor (R-PTP-N) (PTP IA-2)  
 DE (Islet cell antigen 512) (ICA 512) (Islet cell autoantigen 3).  
 GN PTPN OR ICA3 OR ICA512.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94296553; PubMed=8024693;  
 RM Lan M.S., Lu J., Goto Y., Nockins A.L.;  
 RT "Molecular cloning and identification of a receptor-type protein  
 tyrosine phosphatase, IA-2, from human insulinoma.";  
 RL DNA Cell Biol. 13:505-514(1994).  
 RN [2]  
 RP PRELIMINARY SEQUENCE OF 389-789 FROM N.A.  
 RC TISSUE=Pancreatic islets;  
 RA Rabin D.U., Pleasic S.M., Shapero J.A., Yoo-Warren H., Oles J.,  
 Hicks J.M., Goldstein D.R., Rae P.M.;  
 RT "Islet cell antigen 512 is a diabetes-specific islet autoantigen  
 related to protein tyrosine phosphatases.";  
 RL J. Immunol. 152:3183-3188(1994).  
 RN [3]  
 RP REVISIONS TO RSP.2, AND AUTOIMMUNITY IN TYPE I DIABETES.  
 RA MEDLINE=96208497; PubMed=8641276;  
 RM Solimena M., Dirckx R. Jr., Hermel J.-M., Pleasic-Williams S.,  
 Shapero J.A., Caron L., Rabin D.U.;  
 RT "ICA 512, an autoantigen of type I diabetes, is an intrinsic membrane  
 protein of neurosecretory granules.";  
 RL EMBO J. 15:2102-2114(1996).  
 RN [4]  
 RP INTERACTION WITH SNTB2.  
 RA MEDLINE=21376049; PubMed=11483505;  
 RM Ort T., Voronov S., Guo J., Zawalich K., Froehner S.C., Zawalich M.,  
 Solimena M.;  
 RT "Dephosphorylation of beta2-syntrophin and Ca2+/mu-calpain-mediated  
 cleavage of ICA512 upon stimulation of insulin secretion.";  
 RL EMBO J. 20:4013-4023(2001).  
 CC [1] FUNCTION: Implicated in neuroendocrine secretory processes. May be  
 involved in processes specific for neurosecretory granules, such  
 as their biogenesis, trafficking or regulated exocytosis or may  
 have a general role in neuroendocrine functions. Seems to lack  
 intrinsic enzyme activity. May play a role in the regulation of  
 secretory granules via its interaction with SNTB2.  
 CC [2] SUBUNIT: Interacts with phosphorylated SNTB2, protecting it from  
 protein cleavage by CAPN1. Dephosphorylation of SNTB2 upon insulin  
 stimulation disrupts the interaction and results in its cleavage.  
 CC [3] SUBCELLULAR LOCATION: Type I membrane protein. Neuroendocrine  
 secretory granules.  
 CC [4] TISSUE SPECIFICITY: Expression is restricted to neuroendocrine  
 cells. Found in pancreas, brain and pituitary.  
 CC [5] PTM: Appears to undergo multiple proteolytic cleavage at  
 consecutive basic residues.  
 CC [6] DISEASE: Autoantigen in insulin-dependent diabetes mellitus  
 (IDDM).  
 CC [7] SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; L18983; AAA90974.1; -  
 DR EMBL; X62899; CAA44688.2; -

DR HSP: Q06124; 2SHB.  
 DR Genes: HGNC:9676; PTPRN.  
 DR MIM: 601773.  
 DR GO: GO:0005887; C integral to plasma membrane; TAS.  
 DR GO: GO:0005001; P:transmembrane receptor protein tyrosine pho. . . ; TAS.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Receptor; Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 34  
 FT CHAIN 35 979  
 FT DOMAIN 35 575  
 FT TRANSMEM 576 600  
 FT DOMAIN 601 979  
 FT DOMAIN 696 979  
 FT ACT\_SITE 909 909  
 FT SITE 448 449  
 FT CARBOHYD 506 506  
 FT CARBOHYD 524 524  
 SQ SEQUENCE 979 AA; A852B9063D29399D CRC64;  
 Query Match 2.0%; Score 8; DB 1; Length 979;  
 Best Local Similarity 100.0%; Pred. NO. 6.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGPL 238  
 DB 780 YIATQGPL 787  
 RESULT 50  
 PTPN MOUSE STANDARD; PRT; 979 AA.  
 AC Q06073; Q62129;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase-like N precursor (R-PTP-N) (PTP IA-2).  
 GN PTPN OR PTP35.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RX MEDLINE=95071416; PubMed=7980563;  
 RA Lu J., Notkins A.L., Lan M.S.;  
 RT "Isolation, sequence and expression of a novel mouse brain cDNA,  
 RT phosphatase family.";  
 RL Biochem. Biophys. Res. Commun. 204:930-936(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Swiss Webster; TISSUE=Fibroblast;  
 RX MEDLINE=96095652; PubMed=8526904;  
 RA Magistrelli G., Covini N., Mosca M., Lippoli G., Isacchi A.;  
 RT "Expression of PTP35, the murine homologue of the protein tyrosine  
 RT phosphatase-related sequence IA-2, is regulated during cell growth  
 RT and stimulated by mitogens in 3T3 fibroblasts.";  
 RL Biochem. Biophys. Res. Commun. 217:154-161(1995).  
 CC -1- FUNCTION: Implicated in neuroendocrine secretory processes. May be  
 CC involved in processes specific for neurosecretory granules, such  
 CC as their biogenesis, trafficking or regulated exocytosis or may  
 CC have a general role in neuroendocrine functions. Seems to lack  
 CC intrinsic enzyme activity. May play a role in the regulation of  
 CC secretory granules via its interaction with SNTB2 (by similarity).  
 CC  
 CC -1- SUBUNIT: Interacts with phosphorylated SNTB2, protecting it from  
 CC protein cleavage by CAPN1. Dephosphorylation of SNTB2 upon insulin  
 CC stimulation disrupts the interaction and results in its cleavage  
 CC (by similarity).  
 CC  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC  
 CC -1- TISSUE SPECIFICITY: Abundantly expressed in the brain and  
 CC fibroblasts. Weakly expressed in the colon, intestine, stomach and  
 CC pancreas.  
 CC  
 CC -1- DEVELOPMENTAL STAGE: In fibroblasts, maximally expressed in  
 CC exponentially growing cells (days 1 to 4).  
 CC  
 CC -1- INDUCTION: By mitogens such as basic fibroblast growth factor  
 CC (bFGF) and platelet derived growth factor (PDGF).  
 CC  
 CC -1- PTM: Appears to undergo multiple proteolytic cleavage at  
 CC consecutive basic residues (by similarity).  
 CC  
 CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.  
 CC  
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 CC  
 CC EMBL: U1812; AAA52102.1; -;  
 CC EMBL: X74438; CAA52453.1; ALT\_INIT.  
 CC FIR: JC2349; JC2349.  
 CC HSP: P29350; IGWZ.  
 CC MGD: MGI:102765; Ptpn.  
 CC InterPro: IPR000387; TYR\_phosphatase.  
 CC InterPro: IPR000242; Tyr\_PP.  
 CC Pfam: PF00102; Y\_phosphatase; 1.  
 CC PRINTS: PR00700; PRTYPHPTASE.  
 CC SMART: SM00194; PTPC; 1.  
 CC PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 CC PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 CC PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Receptor; Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 37  
 FT CHAIN 38 979  
 FT DOMAIN 38 575  
 FT TRANSMEM 576 600  
 FT DOMAIN 601 979  
 FT DOMAIN 696 979  
 FT ACT\_SITE 909 909  
 FT SITE 448 449  
 FT CARBOHYD 506 506  
 FT CARBOHYD 524 524  
 FT CONFLICT 166 169  
 FT CONFLICT 263 263  
 FT CONFLICT 615 615  
 FT CONFLICT 675 675  
 FT CONFLICT 859 859  
 SQ SEQUENCE 979 AA; 106087 MW; 99921701B202B8C3 CRC64;  
 Query Match 2.0%; Score 8; DB 1; Length 979;  
 Best Local Similarity 100.0%; Pred. NO. 6.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGPL 238  
 DB 780 YIATQGPL 787  
 RESULT 51  
 PTPN RAT STANDARD; PRT; 983 AA.  
 ID PTPN RAT  
 AC Q63259; Q62883; Q63795; Q64643;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase-like N precursor (R-PTP-N) (105 kDa islet

DE cell antigen) (IC105) (PTP IA-2) (PBLP) (Brain-enriched membrane-associated protein tyrosine phosphatase) (BEM-3).

OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

NCBI\_TaxID=10116;

SEQUENCE FROM N.A.

MEDLINE=96016179; PubMed=7568143;

Pasini N., Larigan J.D., Genovese S., Appella E., Sinigaglia F., Rogge L.

"The 37/40-kilodalton autoantigen in insulin-dependent diabetes mellitus is the putative tyrosine phosphatase IA-2."

Proc. Natl. Acad. Sci. U.S.A. 92:9412-9416(1995).

(2)

SEQUENCE OF 13-983 FROM N.A.

STRAIN=Sprague-Dawley; TISSUE=Brain;

MEDLINE=95386708; PubMed=757822;

Payton M.A., Hawkes C.J., Christie M.R.

"Relationship of the 37,000- and 40,000-M(r) tryptic fragments of islet antigens in insulin-dependent diabetes to the protein tyrosine phosphatase-like molecule IA-2 (ICAS12)."

3. Clin. Invest. 96:1506-1511(1995).

(3)

SEQUENCE FROM N.A.

MEDLINE=95194305; PubMed=7887886;

Kamayashi Y., Takahashi K., Sathian S., Inagami T.

"Cloning and expression of protein tyrosine phosphatase-like protein derived from a rat pheochromocytoma cell line."

Biochem. J. 306:331-335(1995).

(4)

SEQUENCE OF 396-983 FROM N.A.

STRAIN=WiStar; TISSUE=Brain;

Itoh S., Okada M., Nakagawa H.

Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

FUNCTION: Implicated in neuroendocrine secretory processes. May be involved in processes specific for neurosecretory granules, such as their biogenesis, trafficking or regulated exocytosis or may have a general role in neuroendocrine functions. Seems to lack intrinsic enzyme activity. May function as a negative regulator of proteases in neuronal tissues. May play a role in the regulation of secretory granules via its interaction with SNTB2 (by similarity).

SUBUNIT: Interacts with phosphorylated SNTB2, protecting it from protein cleavage by CAPN1. Dephosphorylation of SNTB2 upon insulin stimulation disrupts the interaction and results in its cleavage (by similarity).

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed only in brain, specifically in cerebral cortex, diencephalon and brain stem.

INDUCTION: By mitogens such as basic fibroblast growth factor (bFGF) and platelet derived growth factor (PDGF) (by similarity).

PTM: Appears to undergo multiple proteolytic cleavage at consecutive basic residues (by similarity).

SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.

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EMBL: X92563; CAA63313.1; -

EMBL: U40652; AA83235.1; -

EMBL: D38222; BAA07397.1; -

EMBL: D45414; BAA08254.1; -

HSSP: Q06124; 2SHP.

InterPro: IPR000387; TYR phosphatase.

InterPro: IPR000242; TYR PP.

Pfam: PF00102; Y phosphatase; 1.

PRINTS; PR00700; PRTPPHPTASE.

SMART; SM00194; PTPC; 1.

PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.

PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.

PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.

KW Receptor; Glycoprotein; Signal; Transmembrane.

FT SIGNAL 1 40

FT CHAIN 41 983

FT DOMAIN 41 579

FT TRANSMEM 580 604

FT DOMAIN 605 983

FT DOMAIN 700 983

FT ACT\_SITE 913 913

FT SITE 452 453

FT CARBOHYD 510 510

FT CARBOHYD 528 528

FT CONFLICT 1 101

FT CONFLICT 466 466

FT CONFLICT 507 507

FT CONFLICT 517 517

FT CONFLICT 520 520

FT CONFLICT 564 564

FT CONFLICT 566 566

FT CONFLICT 574 574

FT CONFLICT 581 581

FT CONFLICT 599 599

FT CONFLICT 609 609

FT CONFLICT 664 664

FT CONFLICT 672 672

FT CONFLICT 714 714

FT CONFLICT 716 716

FT CONFLICT 731 731

FT CONFLICT 953 953

FT CONFLICT 962 962

FT CONFLICT 966 966

FT CONFLICT 969 969

FT CONFLICT 971 971

FT CONFLICT 976 976

FT CONFLICT 983 AA; 106227 MW; BCD567DAFFFE2A2B CRC64;

SEQUENCE

Query Match 2.0%; Score 8; DB 1; Length 983;

Best Local Similarity 100.0%; Pred.No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 231 YIATQGPL 238

Db 784 YIATQGPL 791

RESULT 52

PT07 STYPL

ID PT07 STYPL STANDARD; PRT; 112 AA.

AC P28199;

01-DEC-1992 (Rel. 24, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Protein-tyrosine phosphatase 7 (EC 3.1.3.48) (Fragment).

GN STY 7.

OS Styela plicata (Sea squirt).

OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;

OC Stolidobranchia; Styelidae; Styela.

OC NCBI\_TaxID=7726;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=91139172; PubMed=1704870;

RA Matthews R.J., Flores E., Thomas M.L.;

RT "Protein tyrosine phosphatase domains from the protochordate Styela plicata."

RL Immunogenetics 33:33-41(1991).

RN [2]



RP REVISIONS TO C-TERMINUS.  
RA Matthews R.J., Flores E., Thomas M.L.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
CC tyrosine + phosphate.  
CC  
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CC  
CC EMBL; M37992; AAA29825.1; -.  
DR HSSP; P28827; IRPM.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PS00700; PRTVPHPTASE.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; PARTIAL.  
DR PROSITE; PS00566; TYR\_PHOSPHATASE\_2; PARTIAL.  
DR PROSITE; PS00565; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.  
FT NON\_TER 1 1  
FT TER 112 112  
SQ SEQUENCE 112 AA; 13299 MW; 6F19D514C6895D9FC CRC64;  
  
Query Match 1.7%; Score 7; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 327 WPDHGTGP 333  
DB 80 WPDHGTGP 86  
|||||  
  
RESULT 53  
CSF2\_FSLCA  
ID CS22 FELCA STANDARD; PRT; 144 AA.  
AC O62757;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)  
DE (Colony-stimulating factor) (CSF).  
GN CSF2.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hughes K.J., O'Reilly K.L.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytokine that stimulates the growth and differentiation  
CC of hematopoietic precursor cells from various lineages, including  
CC granulocytes, macrophages, eosinophils and erythrocytes (by  
CC similarity).  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GM-CSF family.  
CC  
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CC  
CC EMBL; AF053007; AAC06041.1; -.  
DR HSSP; P04141; 2GMF.

DR InterPro; IPR000773; GM-CSF.  
DR Pfam; PF01109; GM-CSF; 1.  
DR PRINTS; PR00593; GMCSEFACTOR.  
DR ProDom; PD007349; GM-CSF; 1.  
DR SMART; SM00040; CSF2; 1.  
DR PROSITE; PS00702; GM-CSF; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 144  
BY SIMILARITY.  
FT GRANULOCYTE-MACROPHAGE COLONY-STIMULATING  
FT FACTOR.  
FT DISULFID 71 113  
FT BY SIMILARITY.  
FT DISULFID 105 138  
FT BY SIMILARITY.  
FT CARBOHYD 44 44  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 45 45  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 54 54  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 144 AA; 16505 MW; 42CSBF5F8235DA55 CRC64;  
  
Query Match 1.7%; Score 7; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 277 ISLKEPL 283  
DB 88 ISLKEPL 94  
|||||  
  
RESULT 54  
S3DR\_STAM  
ID S3DR\_STAM STANDARD; PRT; 180 AA.  
AC Q93VP8;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Putative 5' (3')-deoxyribonucleotidase (EC 3.1.3.-).  
GN SAV0725 OR SA0680.  
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and  
OS Staphylococcus aureus (strain N315).  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=158878, 158879;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=Mu50 / ATCC 700699, and N315;  
RX MEDLINE=21311952; PubMed=11418146;  
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Imai J.-O., Ito T.,  
RA Kanamori M., Matsunaru H., Murakami H., Hosoyama A.,  
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
RA Kanehisa M., Yanashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
RT aureus.";  
RL Lancet 357:1225-1240 (2001).  
CC -!- FUNCTION: Dephosphorylates the 5' and 2' (3')-phosphates of  
CC deoxyribonucleotides (Potential).  
CC -!- SIMILARITY: Belongs to the 5' (3')-deoxyribonucleotidase family.  
CC  
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CC  
CC EMBL; AP003360; BAB56887.1; -.  
DR EMBL; AP003131; BAB41913.1; -.  
DR PIR; F89844; F89844.  
KW Hypothetical protein; Hydrolase; Complete proteome.  
SQ SEQUENCE 180 AA; 20961 MW; 0C5BC1A658221275 CRC64;  
  
Query Match 1.7%; Score 7; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SFSDKYE 67  
|||||  
Db 98 SFSDKYE 104

RESULT 55  
53DR STAAW STANDARD; PRT; 180 AA.  
AC Q8NKK2;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DE Putative 5' (3')-deoxyribonucleotidase (EC 3.1.3.-).  
GN MW0687.  
OS Staphylococcus aureus (strain MW2).  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=196620;  
RN [1]  
RP SEQUENCE FROM N.A.  
RK MEDLINE=22040717; PubMed=12044378;  
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
RA Nagai Y., Ikawa M., Asano K., Naimi T., Kuroda H., Cui L.,  
RA Yamamoto K., Hiramatsu K.;  
RT "Genome and virulence determinants of high virulence community-  
acquired MRSA";  
RL Lancet 359:1819-1827(2002).  
CC -!- FUNCTION: Dephosphorylates the 5' and 2'(3')-phosphates of  
deoxyribonucleotides (Potential).  
CC -!- SIMILARITY: Belongs to the 5'(3')-deoxyribonucleotidase family.  
CC  
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CC  
CC EMBL; AF004824; BAB94552.1; --  
KW Hypothetical protein; Hydrolase; Complete proteome.  
SQ SEQUENCE 180 AA; 20987 MW; 11ED077D3C734330 CRC64;  
Query Match 1.7%; Score 7; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SFSDKYE 67  
|||||  
Db 98 SFSDKYE 104

RESULT 56  
Y4XK RHISN STANDARD; PRT; 188 AA.  
ID Y4XK RHISN  
AC P55703;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical lipoprotein Y4XK precursor.  
GN Y4XK.  
OS Rhizobium sp. (strain NGR234).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=294;  
RN [1]  
RP SEQUENCE FROM N.A.  
RK MEDLINE=97305956; PubMed=9163424;  
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
RA Perret X.;  
RT "Molecular basis of symbiosis between Rhizobium and legumes.";

RL Nature 387:394-401(1997).  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
(Probable).  
CC -!- SIMILARITY: None obvious.  
CC  
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CC  
CC EMBL; AB000106; ABA91934.1; --  
DR InterPro; IPR000437; Prok\_lipo\_prot\_S.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Hypothetical protein; Plasmid; Membrane; Lipoprotein; Signal;  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 188 HYPOTHETICAL PROTEIN Y4XK.  
FT LIPID 19 19 N-palmitoyl cysteine (Probable).  
FT LIPID 19 19 S-diacetylglycerol cysteine (Probable).  
SQ SEQUENCE 188 AA; 20592 MW; 650997A67C20D0C1 CRC64;  
Query Match 1.7%; Score 7; DB 1; Length 188;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 SSGSRSL 119  
|||||  
Db 75 SSGSRSL 81

RESULT 57  
SPED PSESM STANDARD; PRT; 264 AA.  
ID SPED PSESM  
AC Q89Z9; 2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)  
(SAMDC) [Contains: S-adenosylmethionine decarboxylase beta chain; S-  
adenosylmethionine decarboxylase alpha chain].  
GN SPED OR SPOT00598.  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DC3000;  
RX MEDLINE=22834015; PubMed=12928499;  
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,  
RA Winn M.L., Dodson R.J., Deboy K.T., Durkin A.S., Kolonay J.F.,  
RA Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,  
RA Nelson W.C., Davidse T., Brinkac L., Zhou L., Liu J., Yuan Q.,  
RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,  
RA Khan S.E., Feldblyum T.V., D'Ascenzo M., Beng W.-L., Ramos A.R.,  
RA Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,  
RA Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,  
RA White O., Fraser C.M., Collmer A.;  
RT "The complete genome sequence of the Arabidopsis and tomato pathogen  
Pseudomonas syringae pv. tomato DC3000.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).  
CC -!- FUNCTION: Decarboxylation of S-adenosylmethionine provides the  
aminopropyl moiety required for spermidine biosynthesis from  
putrescine (By similarity).  
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-  
adenosyl (3-aminopropyl) methylsulfonium salt + CO(2).  
CC -!- COFACTOR: Pyruvoyl group (By similarity).  
CC -!- SIMILARITY: Belongs to the prokaryotic AdoMetDC family. Subfamily  
2.  
CC

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DR EMBL; AE016858; AA054140.1; -;  
 DR TIGR; PSPT00598; -;  
 DR HAMAP; MF\_00465; -; 1.  
 DR InterPro; IPR003826; SAMDC.  
 DR Pfam; PF02675; AdoMetDC; 1.  
 DR PIRSF; PIRSF01356; SAM decarboxylas; 1.  
 DR Spermidine biosynthesis; lyase; Decarboxylase; Zymogen; Pyruvate;  
 KW Complete proteome. 112  
 FT CHAIN 1 112 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA  
 FT CHAIN 113 264 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA  
 FT SITE 112 113 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).  
 FT MOD\_RES 113 113 CONVERTED TO A PYRUVYL GROUP (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 264 AA; 30347 MW; 05E1C885CAD80292 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 236 GPLPPTI 242  
 DB 100 GPLPPTI 106  
 |||||

RESULT 58  
 Y149 MYCGE STANDARD; PRT; 281 AA.  
 AC P47395;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical lipoprotein MG149 precursor.  
 GN MG149.  
 OS Mycoplasma genitalium.  
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 CC NCBI\_TaxID=2097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=96026346; PubMed=7569993;  
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
 RA Fritchman J.B., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,  
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
 RA Tomb J.-P., Dougherty B.A., Brott K.F., Hu P.-C., Lucier T.S.,  
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  
 RT "The minimal gene complement of Mycoplasma genitalium."  
 RL Science 270:397-403(1995)  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 CC (Potential).

-----  
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DR EMBL; U39696; AAC71367.1; -;  
 DR PIR; E64216; E64216.  
 DR TIGR; MG149; -;  
 DR InterPro; IPR000437; Prok\_lipoprot\_S.

DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 KW Hypothetical protein; Lipoprotein; Membrane; Signal;  
 FT SIGNAL 1 23 Complete proteome; Palmitate.  
 FT CHAIN 24 281 HYPOTHETICAL LIPOPROTEIN MG149.  
 FT LIPID 24 24 N-palmitoyl cysteine (Potential).  
 FT LIPID 24 24 S-diacylglycerol cysteine (Potential).  
 SQ SEQUENCE 281 AA; 32428 MW; AB8628BADD005FF CRC64;

Query Match 1.7%; Score 7; DB 1; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 KEELDII 166  
 DB 261 KEELDII 267  
 |||||

RESULT 59  
 END4 CHLMU STANDARD; PRT; 288 AA.  
 AC Q9PJ88;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).  
 GN NFO OR TC0914.  
 OS Chlamydia muridarum.  
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 CC NCBI\_TaxID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MoPn / Ni99;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Dodson R.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman G., Salzberg S.L.,  
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RT pneumoniae AR39."  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -!- FUNCTION: Endonuclease IV plays a role in DNA repair. It cleaves  
 CC phosphodiester bonds at apurinic or apyrimidinic sites (AP sites)  
 CC to produce new 5' ends that are base-free deoxyribose 5-phosphate  
 CC residues. It preferentially attacks modified AP sites created by  
 CC bleomycin and neocarzinostatin (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
 CC phosphooligonucleotide end-products.  
 CC -!- COFACTOR: Binds 3 zinc ions (By similarity).  
 CC -!- SIMILARITY: Belongs to the AP endonuclease family 2.  
 CC  
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DR EMBL; AE002358; AAF39706.1; -;  
 DR PIR; B81650; B81650.  
 DR HSSP; P12638; IQUM.  
 DR TIGR; TC0914; -;  
 DR HAMAP; MF\_00152; -; 1.  
 DR InterPro; IPR001719; AP endonuclease2.  
 DR Pfam; PF01261; AP\_endonuc\_2; 1.  
 DR SMART; SM00518; AP2EC; 1.  
 DR TIGRFAMs; TIGR00587; nfo; 1.  
 DR PROSITE; PS00729; AP\_NUCLEASE\_P2\_1; 1.  
 DR PROSITE; PS00730; AP\_NUCLEASE\_P2\_2; 1.  
 DR PROSITE; PS00731; AP\_NUCLEASE\_P2\_3; 1.  
 KW Hydrolase; Nuclease; Endonuclease; DNA repair; Metal-binding; Zinc;

```

KW Complete proteome.
FT METAL 75
FT METAL 115
FT METAL 153
FT METAL 187
FT METAL 190
FT METAL 224
FT METAL 237
FT METAL 239
FT METAL 269
SQ SEQUENCE 288 AA; 31013 MW; 118553A1849C399 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 PEGNKKD 213
DB 231 PEGNKKD 237

RESULT 60
YDAO HAEIN
ID YDAO HAEIN STANDARD; PRT; 313 AA.
AC Q57184; Q05059;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H1371.1.
GN H1371.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=127;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD.";
RL Science 269:496-512(1995).
RN [2]
RP REVISIONS.
RA White O., Clayton R.A., Kervatage A.R., Fleischmann R.D.;
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO E.COLI YDAO.
CC
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CC -----
CC EMBL; U32817; AAC23019.1; -.
CC TIGR; H1371.1; -.
CC KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 313 AA; 35703 MW; 64617CB802F7252 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 130 ELTOLAQ 136
DB 3 ELTOLAQ 9

RESULT 61
SYW CAUCR
ID SYW CAUCR STANDARD; PRT; 344 AA.
AC Q9AC05;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
DE (TPRS).
GN TRPS OR CC0064.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.P., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.P., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminocyl-tRNA synthetase family.
CC
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CC -----
CC EMBL; AE005680; AAK22051.1; -.
CC PIR; G87256; G87256.
CC HSSP; P00953; 1D2R.
CC TIGR; CC0064; -.
CC HAMAP; MF_00140; -.
CC InterPro; IPR002305; tRNA-synt_1b.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002306; Trp tRNA-synt_1b.
CC Pfam; PF00579; tRNA-synt_1b; 1.
CC PRINTS; PR01039; TRNASYNTHTRP.
CC TIGRFAMs; TIGR00233; trps; 1.
CC PROSITE; PS00178; AA tRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
FT SITE 21 29 "HIGH" REGION.
FT SITE 206 210 "KMSKS" REGION.
FT BINDING 209 209 ATP (BY SIMILARITY).
SQ SEQUENCE 344 AA; 37151 MW; C9B45E76FB49D34 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 237 PUFETIE 243
DB 240 PUFETIE 246

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RESULT 62  
 DDLA\_PSEPK STANDARD; PRT; 352 AA.  
 AC Q88EV6;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE D-alanine-D-alanine ligase A (EC 6.3.2.4) (D-alanylanine synthetase A) (D-Ala-D-Ala ligase A).  
 GN DDLA OR PP4346.  
 OS Pseudomonas putida (strain KT2440).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=160488;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22423060; PubMed=12534453;  
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,  
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,  
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,  
 RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Medler H.,  
 RA Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,  
 RA Kiewitz C., Eisen J., Flumis K.N., Duesterhoeft A., Tuemmler B.,  
 RA Fraser C.M.;  
 RT "Complete genome sequence and comparative analysis of the  
 RT metabolically versatile Pseudomonas putida KT2440.";  
 RL Environ. Microbiol. 4:799-808(2002).  
 CC -1- FUNCTION: Cell wall formation (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + D-alanyl-D-alanine  
 CC -1- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second  
 CC step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.  
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 CC -----  
 DR EMBL; AE016790; AAN69925.1; -;  
 DR TIGR; PP4346; -;  
 DR HAMAP; MF\_00047; -; 1.  
 DR InterPro; IPR000291; Dala\_lig\_Van.  
 DR Pfam; PF01820; Dala\_Dala\_Ligase; 1.  
 DR PROSITE; PS00843; DALA\_DALA\_LIGASE\_1; 1.  
 DR PROSITE; PS00844; DALA\_DALA\_LIGASE\_2; 1.  
 DR Ligase; Cell wall; Peptidoglycan synthesis; Complete proteome.  
 SK SEQUENCE 352 AA; 37804 MW; 51FA8522FD896BB1 CRC64;  
 CC -----  
 Query Match 1.7%; Score 7; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 262 REIECGV 268  
 Db 217 REIECGV 223  
 [|||||]  
 RESULT 63  
 PTN7\_RAT STANDARD; PRT; 359 AA.  
 AC P49445;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase, non-receptor type 7 (EC 3.1.3.48)

(Protein-tyrosine phosphatase LC-PTP) (Hematopoietic protein-tyrosine phosphatase) (HEPTP).  
 GN PTN7.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=95394959; PubMed=7545170;  
 RA Swieter M., Berenstein E.H., Swaim W.D., Siraganian R.P.;  
 RT "Aggregation of IGE receptors in rat basophilic leukemia 2H3 cells  
 RT induces tyrosine phosphorylation of the cytosolic protein-tyrosine  
 RT phosphatase HePTP.";  
 RL J. Biol. Chem. 270:21902-21906(1995).  
 CC -1- FUNCTION: May play a role in the regulation of T and B lymphocyte  
 CC development and signal transduction (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; U28356; AAB84443.1; -;  
 DR HSPF; P29350; IGWZ.  
 DR InterPro; IPR008356; KIM\_Tyr\_phosph.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PK01778; KIMTPPASE.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00096; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolase.  
 KW DOMAIN 119 342 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 290 290 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 FT SEQUENCE 359 AA; 40314 MW; 5B98E196DB633677 CRC64;  
 CC -----  
 Query Match 1.7%; Score 7; DB 1; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGP 237  
 Db 165 YIATQGP 171  
 [|||||]  
 RESULT 64  
 PTN7\_HUMAN STANDARD; PRT; 360 AA.  
 AC P35236; Q9BV05;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Protein-tyrosine phosphatase, non-receptor type 7 (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase LC-PTP) (Hematopoietic protein-tyrosine  
 DE phosphatase) (HEPTP).  
 GN PTN7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;



DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.  
 FT DOMAIN 118 361 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 300 300 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 SIMILARITY).  
 SQ SEQUENCE 369 AA; 42366 MW; 7CD8A77EB238C64B CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 7; DB 1; Length 369;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 VIATQGP 237  
 DB 173 VIATQGP 179

RESULT 66  
 ID PTP2\_DICDI STANDARD; PRT; 377 AA.  
 AC P34138;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Protein-tyrosine phosphatase 2 (EC 3.1.3.48) (Protein-tyrosine-  
 phosphate phosphohydrolase 2) (PTPA).  
 GN PTPB OR PTP2.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX4;  
 RX MEDLINE=94043028; PubMed=8226777;  
 RA Ramalingam R., Shaw D.R., Ennis H.;  
 RT "Cloning and functional expression of a Dictyostelium discoideum  
 protein tyrosine phosphatase.";  
 RL J. Biol. Chem. 268:22680-22685 (1993).  
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 tyrosine + phosphate.  
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Non-receptor class subfamily.  
 CC  
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 CC  
 CC EMBL; L15420; AAA33242.1; -;  
 CC PIR; A48711; A48711.  
 CC HSSP; P18031; 2HNQ.  
 CC DictyBase; DB0002003; ptpB.  
 CC InterPro; IPR000387; TYR\_PTPase.  
 CC InterPro; IPR00242; TYR\_PP.  
 CC Pfam; PF00102; Y\_phosphatase; 1.  
 CC FRANT; PRO0700; PRTYPHPTASE.  
 CC SMART; SM00194; PTPC; 1.  
 CC PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
 CC PROSITE; PS00056; TYR\_PHOSPHATASE 2; 1.  
 CC PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.  
 FT DOMAIN 78 86 POLY-ASP.  
 FT DOMAIN 95 103 POLY-ASN.  
 FT ACT\_SITE 281 281 PHOSPHOCYSTEINE INTERMEDIATE (BY  
 SIMILARITY).  
 SQ SEQUENCE 377 AA; 43488 MW; 5B0BF6EB54829FD9 CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 7; DB 1; Length 377;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 327 WPDHGTP 333  
 DB 249 WPDHGTP 255

RESULT 67  
 ID DDL\_STRAW STANDARD; PRT; 385 AA.  
 AC Q82J55;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE D-alanine-D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase)  
 DE (D-Ala-D-Ala ligase).  
 GN DDL OR DDLA OR SAV2679.  
 OS Streptomyces avermitilis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=33903;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
 RX MEDLINE=21477403; PubMed=11572948;  
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
 RA Shinose M., Takahashi Y., Horioka H., Nakazawa H., Osonoe T.,  
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
 RT "Genome sequence of an industrial microorganism Streptomyces  
 avermitilis: deducing the ability of producing secondary  
 metabolites.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
 RX MEDLINE=22608306; PubMed=12692562;  
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
 RA Sakaki Y., Hattori M., Omura S.;  
 RT "Complete genome sequence and comparative analysis of the industrial  
 microorganism Streptomyces avermitilis.";  
 RL Nat. Biotechnol. 21:526-531 (2003).  
 CC -!- FUNCTION: Cell wall formation (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-  
 alanyl-D-alanine.  
 CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second  
 step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the D-alanine-D-alanine ligase family.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AP005031; BAC70390.1; -;  
 CC HAMAP; MF\_00047; -; 1.  
 CC InterPro; IPR000291; Dala\_lig\_Van.  
 CC InterPro; IPR005905; D\_alal\_Dala.  
 CC Pfam; PF01820; Dala\_Dala\_ligase; 1.  
 CC TIGRFAMs; TIGR01205; D\_alal\_D\_alalTIGR; 1.  
 CC PROSITE; PS00843; DALA\_DALA\_LIGASE 1; 1.  
 CC PROSITE; PS00844; DALA\_DALA\_LIGASE 2; FALSE\_NEG.  
 KW Ligase; Cell wall; Peptidoglycan synthesis; Complete proteome.  
 SQ SEQUENCE 385 AA; 41905 MW; 2674F3517D4FAE79 CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 7; DB 1; Length 385;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 REIECGV 268  
 DB 253 REIECGV 259

```

RESULT 68
DDL_STRCO          STANDARD;          PRT;    389 AA.
AC  Q9Z8R9;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  D-alanine--D-alanine ligase (BC 6.3.2.4) (D-alanylanine synthetase)
DE  (D-Ala-D-Ala ligase)
GN  DDL OR DDLA OR SCO5560 OR SCTA1.04.
OS  Streptomyces coelicolor.
OC  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC  Streptomycineae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxID=1902;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21996410; PubMed=12000953;
RA  Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA  Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA  Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA  Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA  Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA  Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA  Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA  Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA  Hopwood D.A.;
RT  "Complete genome sequence of the model actinomycete Streptomyces
RT  coelicolor A3(2).";
RL  Nature 417:141-147(2002).
CC  -!- FUNCTION: Cell wall formation (By similarity).
CC  -!- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
CC  alanyl-D-alanine.
CC  -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
CC  step.
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -!- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AL939124; CAA22403.1; -
CC  PIR; T35644; T35644.
CC  HSP; P07862; 110W.
CC  HAMAP; MF 00047; -; 1.
CC  InterPro; IPR005905; D_alA_D_alA.
CC  InterPro; IPR000291; Dala_Lig_Van.
CC  Pfam; PF01820; Dala-Dala_ligas; 1.
CC  TIGRfam; TIGR01205; D_alA_D_alatIGR; 1.
CC  PROSITE; PS00843; DALA_DALA_LIGASE_1; 1.
CC  PROSITE; PS00844; DALA_DALA_LIGASE_2; FALSE NEG.
KW  Ligase; Cell wall; Peptidoglycan synthesis; Complete proteome.
SQ  SEQUENCE 389 AA; 42272 MW; 9F25CE27B761DP49 CRC64;

Query Match          1.7%; Score 7; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  262 REIEGV 268
    |||||
DB  257 REIEGV 263

RESULT 69
EFTU_XYLF
ID  EFTU_XYLF          STANDARD;          PRT;    395 AA.
AC  Q877P8;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Elongation factor Tu (EF-Tu).
DE  (TUFA OR PD1996) AND (TUFB OR PD2009).
GN  Xylella fastidiosa (strain Temecula) / ATCC 700964.
OS  Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC  Xanthomonadaceae; Xylella.
OX  NCBI_TaxID=183190;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22421331; PubMed=12533478;
RA  Van Slyke M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA  Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA  Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA  Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorfy H., Teai S.M.,
RA  Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA  Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA  Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA  Baia G.S., Blanco S.R., Brito M.S., Camavan F.S., Celestino A.V.,
RA  da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA  Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA  de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA  Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA  Kitajima J.P.;
RT  "Comparative analyses of the complete genome sequences of Pierce's
RT  disease and citrus variegated chlorosis strains of Xylella
RT  fastidiosa";
RL  J. Bacteriol. 185:1018-1026(2003).
CC  -!- FUNCTION: This protein promotes the GTP-dependent binding of
CC  aminoacyl-tRNA to the A-site of ribosomes during protein
CC  biosynthesis.
CC  -!- SUBUNIT: Monomer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC  EF-Tu/EF-1a subfamily.
CC  -----
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CC  -----
CC  EMBL; AE012560; RAO29825.1; -
CC  EMBL; AE012560; RAO29837.1; -
CC  HAMAP; MF 00118; -; 1.
CC  InterPro; IPR004541; EF-Tu.
CC  InterPro; IPR000795; EF_GTPbind.
CC  InterPro; IPR004160; EFTU_Cterm.
CC  InterPro; IPR004161; EFTU_D2.
CC  InterPro; IPR009001; Elong_init_C.
CC  InterPro; IPR005225; Small_GTP.
CC  InterPro; IPR009000; Translat_factor.
CC  Pfam; PF00009; GTP_EFTU; 1.
CC  Pfam; PF03144; GTP_EFTU_D2; 1.
CC  Pfam; PF03143; GTP_EFTU_D3; 1.
CC  PRINTS; PR00315; ELONGATWCT.
CC  TIGRfam; TIGR00485; EF-Tu; 1.
CC  TIGRfam; TIGR00231; small_GTP; 1.
CC  PROSITE; PS00301; EFACOR_GTP; 1.
KW  Elongation factor; Protein biosynthesis; GTP-binding;
KW  Complete proteome.
FT  INIT MET 0 0 BY SIMILARITY.
FT  NP_BIND 18 25 GTP (BY SIMILARITY).
FT  NP_BIND 80 84 GTP (BY SIMILARITY).
FT  NP_BIND 135 138 GTP (BY SIMILARITY).
SQ  SEQUENCE 395 AA; 42775 MW; 02DFDF4FB60A50 CRC64;

Query Match          1.7%; Score 7; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 30;

```



Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 IECGVIK 270  
 Db 233 IECGVIK 239

RESULT 70  
 G59F\_DROME STANDARD; PRT; 406 AA.

AC Q9WNS;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Putative gustatory receptor 59f.  
 GN GR59F OR GR59E.1 OR CG10185/CG5365.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CX NCBI\_taxID=7227;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galie R.P.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.I., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster.";  
 RT Science 287:2185-2195(2000).  
 RL [2]

REVIEWS:  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Bradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.I., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;

"Annotation of the Drosophila melanogaster euchromatic genome: a  
 systematic review.";  
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RL [3]  
 RN IDENTIFICATION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=20175760; PubMed=10710312;  
 RA Clyne P.J., Warr C.G., Carlson J.R.;  
 RT "Candidate taste receptors in Drosophila.";  
 RL Science 287:1830-1834(2000).  
 RN [4]  
 RN IDENTIFICATION.  
 RX MEDLINE=21407712; PubMed=11516643;  
 RA Dunipace L., Meister S., McNeely C., Amrein H.;  
 RT "Spatially restricted expression of candidate taste receptors in the  
 Drosophila gustatory system.";  
 RL Curr. Biol. 11:822-835(2001).  
 RN [5]  
 RN CONCEPTUAL TRANSLATION.  
 RA Robertson H.;  
 RL Unpublished observations (NOV-2001).  
 CC -!- FUNCTION: Probable role in the gustatory response.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Expressed in the adult abdomen and wing.  
 CC -!- SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED  
 CC RECEPTORS. SUBFAMILY VIII.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC -----  
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 CC -----  
 CC FLYBASE; AB003461; AAF47022.2; ALT\_SEQ.  
 DR FLYBASE; FBgn0041234; Gr59f.  
 DR GO; GO:0016021; C:integral to membrane; NAS.  
 DR GO; GO:0008527; F:taste receptor activity; NAS.  
 DR GO; GO:0007697; P:taste; NAS.  
 DR Hypothetical protein; Receptor; G-protein coupled receptor;  
 KW Transmembrane; Glycoprotein; Multigene family.  
 FT TRANSMEM 1 36  
 FT DOMAIN 37 57  
 FT DOMAIN 58 69  
 FT TRANSMEM 70 90  
 FT DOMAIN 91 99  
 FT TRANSMEM 100 120  
 FT DOMAIN 121 154  
 FT TRANSMEM 155 175  
 FT DOMAIN 176 189  
 FT TRANSMEM 190 210  
 FT DOMAIN 211 259  
 FT TRANSMEM 260 280  
 FT DOMAIN 281 364  
 FT TRANSMEM 365 385  
 FT DOMAIN 386 406  
 FT CARBOHYD 315 315  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 406 AA; 47559 MW; 7548A5A2F2465614 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 334 ASADFFI 340  
 Db 376 ASADFFI 382  
 |||||  
 |||||

RESULT 71  
 PEPT\_LACHE  
 ID -PEPT\_LACHE STANDARD; PRT; 413 AA.

AC Q9L4G1;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Peptidase T (EC 3.4.11.14) (Tripeptide aminopeptidase)  
 DE (Aminotripeptidase) (Tripeptidase).  
 GN PEST.  
 OS Lactobacillus helveticus.  
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 CC Lactobacillus.  
 CC NCBI\_TaxID=1587;  
 OX [1]  
 RN  
 RP SEQUENCE FROM N.A., SEQUENCE OF 1-17, AND CHARACTERIZATION.  
 RC STRAIN=53/7;  
 RX MEDLINE=20120540; PubMed=10653753;  
 RA Savijoki K., Palva A.;  
 RT "Purification and molecular characterization of a tripeptidase from  
 RL Lactobacillus helveticus.";  
 RL Appl. Environ. Microbiol. 66:794-800(2000).  
 CC !- FUNCTION: Release the N-terminal amino acid from tripeptides. Has  
 CC a preference for tripeptides containing a N-terminal methionine or  
 CC leucine.  
 CC !- CATALYTIC ACTIVITY: Release of a N-terminal residue from a  
 CC tripeptide.  
 CC !- COFACTOR: Zinc.  
 CC !- SUBUNIT: Homotrimer (Probable).  
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC !- SIMILARITY: Belongs to peptidase family M20A.  
 CC !- CAUTION: The potential zinc-binding site Asp residue in position  
 CC 144 is replaced by a Met.  
 CC  
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 CC  
 DR EMBL; AJ243321; CAB72938.1; -.  
 DR HAMAP; MF 00550; atypical; 1.  
 DR InterPro; IPR002933; Peptidase M20.  
 DR Pfam; PF01546; Peptidase\_M20; 1.  
 KW Hydrolase; Aminopeptidase; Metalloprotease; Zinc.  
 FT METAL 82 82 ZINC (BY SIMILARITY).  
 FT METAL 201 201 ZINC (BY SIMILARITY).  
 SQ SEQUENCE 413 AA; 46681 MW; 2A55363A0DA60952 CRC64;  
 Query Match 1.7%; Score 7; DB 1; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 50 NSENVKP 56  
 DB 89 NSENVKP 95  
 RESULT 72  
 V1AR\_SHEEP  
 ID V1AR\_SHEEP STANDARD; PRT; 418 AA.  
 AC P48043;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Vasopressin Via receptor (V1AR) (Vascular/hepatic-type arginine  
 DE vasopressin receptor) (Antidiuretic hormone receptor 1a) (AVPR V1a).  
 GN AVPR1A  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis.  
 CC NCBI\_TaxID=9940;  
 OX [1]  
 RN

RP SEQUENCE FROM N.A.  
 RX MEDLINE=96004901; PubMed=7548217;  
 RA Hutchins A.-M., Phillips P.A., Venter D.J., Burrell L.M.,  
 RA Johnston C.I.;  
 RT "Molecular cloning and sequencing of the gene encoding a sheep  
 RT arginine vasopressin type 1a receptor.";  
 RL Biochim. Biophys. Acta 1263:266-270(1995).  
 CC !- FUNCTION: Receptor for arginine vasopressin. The activity of this  
 CC receptor is mediated by G proteins which activate a phosphatidyli-  
 CC inositol-calcium second messenger system.  
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC !- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 DR EMBL; L41502; AAC41628.1; -.  
 DR EMBL; L41502; AAC41627.1; ALT\_INIT.  
 DR PIR; S59601; S59601.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;  
 KW Palmitate.  
 FT DOMAIN 1 51 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 52 75 1 (POTENTIAL).  
 FT DOMAIN 76 87 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 88 109 2 (POTENTIAL).  
 FT DOMAIN 110 124 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 125 146 3 (POTENTIAL).  
 FT DOMAIN 147 167 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 168 189 4 (POTENTIAL).  
 FT DOMAIN 190 217 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 218 238 5 (POTENTIAL).  
 FT DOMAIN 239 293 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 294 313 6 (POTENTIAL).  
 FT DOMAIN 314 331 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 332 351 7 (POTENTIAL).  
 FT DOMAIN 352 418 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 123 202 BY SIMILARITY.  
 FT LIPID 365 365 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 13 13 S-palmitoyl cysteine (By similarity).  
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 418 AA; 46521 MW; BDE60C985A6215CE CRC64;  
 Query Match 1.7%; Score 7; DB 1; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 RKVRGKT 11  
 DB 244 RKVRGKT 250  
 RESULT 73  
 ECTB\_MASHA  
 ID ECTB\_MASHA STANDARD; PRT; 427 AA.  
 AC O05050;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Diaminobutyrate--pyruvate aminotransferase (EC 2.6.1.46) (L-  
 DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase).  
 DE NCBI\_TaxID=9940;  
 OX [1]  
 RN

GN ECTB.  
 OS *Marinococcus halophilus*.  
 CC Bacteria; Firmicutes; Bacillales; Sporolactobacillaceae; *Marinococcus*.  
 CC NCBI\_TaxID=1371;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=DSK 20408T;  
 CC MEDLINE=97286530; PubMed=9141677;  
 CC RA Louis P., Galinski E.A.;  
 CC RT "Characterization of genes for the biosynthesis of the compatible  
 CC RT solute ectoine from *Marinococcus halophilus* and osmoregulated  
 CC RT expression in *Escherichia coli*.";  
 CC RL Microbiology 143:1141-1149 (1997).  
 CC CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutanoate + pyruvate = L-  
 CC aspartate 4-semialdehyde + L-alanine.  
 CC CC -1- COFACTOR: Pyridoxal phosphate.  
 CC CC -1- PATHWAY: Biosynthesis of ectoine (1,4,5,6-tetrahydro-2-methyl-4-  
 CC pyrimidine carboxylic acid); first step.  
 CC CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent  
 CC aminotransferases.  
 CC -----  
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 CC -----  
 CC DR EMBL; U66614; AAB57634.1; -.  
 CC DR HSP; P12995; IQJ3.  
 CC DR InterPro; IPR005814; Aminotrans\_3.  
 CC DR InterPro; IPR004637; Dat.  
 CC DR Pfam; PF00202; aminotran\_3; 1.  
 CC DR TIGRFAMs; TIGR00709; dat\_1.  
 CC DR PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; FALSE\_NEG.  
 CC KW Transferase; Aminotransferase; Pyridoxal phosphate.  
 CC SQ SEQUENCE 427 AA; 47193 MW; 907FE135B852EBEF CRC64;  
 CC -----  
 CC Query Match 1.7%; Score 7; DB 1; Length 427;  
 CC Best Local Similarity 100.0%; Pred. No. 33;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Qy 361 AGVGRTG 367  
 CC Db 244 AGVGRTG 250  
 CC [|||||]  
 CC  
 CC RESULT 74  
 CC NQRA\_VIBHA  
 CC ID NQRA\_VIBHA STANDARD; PRT; 446 AA.  
 CC AC Q9RFW1;  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Na(+)-translocating NADH-quinone reductase subunit A (EC 1.6.5.-)  
 CC DE (Na(+)-translocating NQR subunit A) (Na(+)-NQR subunit A) (NQR complex  
 CC DE subunit A) (NQR-1 subunit A).  
 CC GN NQRA.  
 CC OS *Vibrio harveyi*.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 CC Vibrionaceae; *Vibrio*.  
 CC NCBI\_TaxID=669;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=BB120;  
 CC RA MEDLINE=20056044; PubMed=10587447;  
 CC Zhou W., Bertsova Y.V., Feng B., Tsatsos P., Verkhovskaya M.L.,  
 CC Gennis R.B., Bogachev A.V., Barquera B.;  
 CC "Sequencing and preliminary characterization of the Na+-translocating  
 CC NADH:ubiquinone oxidoreductase from *Vibrio harveyi*.";  
 CC RL Biochemistry 38:16246-16252 (1999).  
 CC -1- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to

CC ubiquinol by two successive reactions, coupled with the transport  
 CC of Na(+) ions from the cytoplasm to the periplasm. NQRA to nqrE  
 CC are probably involved in the second step, the conversion of  
 CC ubiquinone to ubiquinol.  
 CC CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +  
 CC ubiquinol + Na(+) (Out).  
 CC CC -1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE  
 CC and nqrF (by similarity).  
 CC CC -1- SIMILARITY: Belongs to the nqrA family.  
 CC -----  
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 CC -----  
 CC DR EMBL; AF165980; AAF15411.1; -.  
 CC DR HAMAP; MF 00425; -; 1.  
 CC DR InterPro; IPR008703; NQRA.  
 CC DR Pfam; PF05896; NQRA; 1.  
 CC KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport.  
 CC SQ SEQUENCE 446 AA; 48365 MW; 9B05B38BBD7A97C CRC64;  
 CC -----  
 CC Query Match 1.7%; Score 7; DB 1; Length 446;  
 CC Best Local Similarity 100.0%; Pred. No. 34;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Qy 30 SLPSSSQ 36  
 CC Db 197 SLPSSSQ 203  
 CC [|||||]  
 CC  
 CC RESULT 75  
 CC EF1A\_ARATH  
 CC ID EF1A\_ARATH STANDARD; PRT; 449 AA.  
 CC AC P13905;  
 CC DT 01-JAN-1990 (Rel. 13, Created)  
 CC DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 CC DE Elongation factor 1-alpha (EF-1-alpha).  
 CC GN AT1G07940 OR T6D22.3) AND (AT5G60390 OR MUF9.4).  
 CC OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 CC NCBI\_TaxID=3702;  
 CC [1]  
 CC RN SEQUENCE FROM N.A. (GENE 1).  
 CC RC STRAIN=cv. Columbia;  
 CC RX MEDLINE=90136496; PubMed=2615757;  
 CC RA Axelos M., Bardet C., Liboz T., le van Thai A., Curie C.,  
 CC RA Lescure B.;  
 CC RT "The gene family encoding the Arabidopsis thaliana translation  
 CC RT elongation factor EF-1 alpha: molecular cloning, characterization and  
 CC RT expression.";  
 CC RL Mol. Gen. Genet. 219:106-112 (1999).  
 CC [2]  
 CC RN SEQUENCE FROM N.A. (GENES 2 AND 3).  
 CC RC STRAIN=cv. Columbia;  
 CC RX MEDLINE=91322484; PubMed=2101309;  
 CC RA Liboz T., Bardet C., le van Thai A., Axelos M., Lescure B.;  
 CC RT "The four members of the gene family encoding the Arabidopsis  
 CC RT thaliana translation elongation factor EF-1 alpha are actively  
 CC RT transcribed.";  
 CC RL Plant Mol. Biol. 14:107-110 (1990).  
 CC [3]  
 CC RN SEQUENCE FROM N.A. (GENES 1; 2 AND 3).  
 CC RC STRAIN=cv. Columbia;  
 CC RA Tremousaygue D., Bardet C., Dabos P., Regad F., Pelese F., Lescure B.;  
 CC RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC [4]

SEQUENCE FROM N.A.  
 RC STRAIN=CV, Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White C., Alonso J., Alcafi H., Araujo R., Bowman C.L., Brooks S.V.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu B., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
 RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RA thaliana."  
 RL Nature 408:815-820(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, Columbia;  
 RX MEDLINE=98344145; PubMed=9679202;  
 RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence  
 RT features of the regions of 1,381,565 bp covered by twenty one  
 RT physically assigned P1 and TAC clones."  
 RL DNA Res. 5:131-145(1998).  
 CC -!- FUNCTION: This protein promotes the GTP-dependent binding of  
 CC aminoacyl-tRNA to the A-site of ribosomes during protein  
 CC biosynthesis.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: There are four genes for EF-1-alpha in Arabidopsis  
 CC thaliana. The sequence of genes 1, 2, and 3 are identical  
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-Tu/EF-1A subfamily.  
 CC  
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 CC  
 CC -----  
 CC EMBL; X16430; CAA34453.1; -  
 CC EMBL; X16431; CAA34454.1; -  
 CC EMBL; X16432; CAA34455.1; -  
 CC EMBL; U63815; AAB07882.1; -  
 CC EMBL; U63815; AAB07883.1; -  
 CC EMBL; U63815; AAB07884.1; -  
 CC EMBL; AC036875; AAF79847.1; -  
 CC EMBL; AB011483; BAB08224.1; -  
 CC PIR; S06724; S06724.  
 CC HSP; P07157; IAP.  
 CC InterPro; IPR004539; EFL alpha.  
 CC InterPro; IPR000795; EF\_GTPbind.  
 CC InterPro; IPR004160; EFTU Cterm.  
 CC InterPro; IPR004161; EFTU D2.  
 CC InterPro; IPR009001; Elong\_init\_C.  
 CC InterPro; IPR009000; Translat\_factor.  
 CC Pfam; PF00009; GTP\_EFTU; 1.  
 CC Pfam; PF03144; GTP\_EFTU D2; 1.  
 CC Pfam; PF03143; GTP\_EFTU D3; 1.  
 CC PRINTS; PR00315; ELONGATNCT.  
 CC TIGRfam; TIGR00483; EF-1 alpha; 1.  
 CC PROSITE; PS00301; BEACTOR\_GTP; 1.  
 KW Elongation factor; Protein biosynthesis; GTP-binding;  
 KW Multigene family.

FT	NP_BIND	14	21	GTP (BY SIMILARITY).
FT	NP_BIND	91	95	GTP (BY SIMILARITY).
FT	NP_BIND	153	156	GTP (BY SIMILARITY).
SQ	SEQUENCE	449 AA;	49502 MW;	12PFA6C537DFCEB9 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 449;  
 Best Local Similarity 100.0%; Pred.No. 34;  
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY	37	KMTPTKP	43
Db	391	KMTPTKP	397

Search completed: June 21, 2004, 17:22:15  
 Job time : 21 secs

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OM protein - protein search, using sw model

Run on: June 21, 2004, 17:20:22 ; Search time 44 Seconds  
(without alignments)

2904.202 Million cell updates/sec

Title: US-09-095-478A-7

Perfect score: 405

Sequence: 1 MSSPRKVRGKTGRDNDREEG.....DIMNIVTQMRKQRCGMQPK 405

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

SPTRMBL 25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_muc.\*
- 8: sp\_organella.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	405	100.0	426	11	O55082	O55082 mus musculus
2	19	4.7	398	4	Q9Y406	Q9Y406 homo sapien
3	15	3.7	336	11	Q9QWQ7	Q9QWQ7 mus musculus
4	15	3.7	446	5	Q9Y1X4	Q9Y1X4 ephydatia f
5	15	3.7	758	11	Q7TWG1	Q7TWG1 mus musculus
6	15	3.7	1024	4	Q8WX29	Q8WX29 homo sapien
7	14	3.5	24	11	O88571	O88571 mus spretus
8	14	3.5	24	11	O88570	O88570 mus musculus
9	14	3.5	79	11	O8CC23	O8CC23 mus musculus
10	14	3.5	93	11	O8CC54	O8CC54 mus musculus
11	14	3.5	134	4	Q9UMZ3	Q9UMZ3 homo sapien
12	14	3.5	183	5	Q9Y1X3	Q9Y1X3 ephydatia f
13	14	3.5	192	11	O8C922	O8C922 mus musculus
14	14	3.5	460	11	O62917	O62917 rattus norv
15	14	3.5	468	13	Q91BA5	Q91BA5 potamotrygo
16	14	3.5	468	13	Q91BA2	Q91BA2 potamotrygo

17	14	3.5	468	13	Q91BA0	Q91BA0 potamotrygo
18	14	3.5	508	13	Q90YJ5	Q90YJ5 brachydanio
19	14	3.5	582	11	Q84696	Q84696 mus musculus
20	14	3.5	615	13	Q91A18	Q91A18 xenopus lae
21	14	3.5	749	11	Q8R169	Q8R169 mus musculus
22	14	3.5	857	13	Q90YJ4	Q90YJ4 brachydanio
23	14	3.5	1191	4	Q7Z3X4	Q7Z3X4 homo sapien
24	14	3.5	1231	5	Q17024	Q17024 anopheles g
25	14	3.5	1254	11	Q8VBV0	Q8VBV0 mus musculus
26	14	3.5	1399	4	O75870	O75870 homo sapien
27	14	3.5	1499	13	Q90815	Q90815 gallus gall
28	14	3.5	1501	11	Q9QWQ0	Q9QWQ0 rattus sp.
29	14	3.5	1501	11	Q7TT17	Q7TT17 mus musculus
30	14	3.5	1502	4	Q9UM81	Q9UM81 homo sapien
31	14	3.5	1788	13	Q91AJ0	Q91AJ0 xenopus lae
32	14	3.5	1863	11	Q84605	Q84605 rattus norv
33	14	3.5	1887	11	Q9QW67	Q9QW67 rattus sp.
34	14	3.5	1894	11	Q84487	Q84487 mus musculus
35	14	3.5	1896	13	Q91AJ1	Q91AJ1 xenopus lae
36	14	3.5	1898	4	Q86WS0	Q86WS0 homo sapien
37	14	3.5	1898	11	Q9EQ17	Q9EQ17 mus musculus
38	14	3.5	1898	11	Q84604	Q84604 r protein-t
39	14	3.5	1904	11	Q84699	Q84699 mus musculus
40	14	3.5	2051	5	O44328	O44328 hirudo medi
41	14	3.5	2302	11	O88488	O88488 rattus norv
42	13	3.2	459	5	Q9NL11	Q9NL11 branchiost
43	13	3.2	469	13	Q9NL08	Q9NL08 eptaretus
44	12	3.0	112	11	Q9ULJ6	Q9ULJ6 mus musculus
45	12	3.0	184	5	O02048	O02048 caenorhabdi
46	12	3.0	361	11	Q61373	Q61373 mus musculus
47	12	3.0	456	5	Q95Y26	Q95Y26 caenorhabdi
48	12	3.0	849	11	Q9ULJ8	Q9ULJ8 mus musculus
49	12	3.0	1168	11	O8CIN1	O8CIN1 rattus norv
50	12	3.0	1216	11	Q82884	Q82884 rattus norv
51	12	3.0	1217	5	O17889	O17889 caenorhabdi
52	12	3.0	1238	11	Q8K3Q2	Q8K3Q2 mus musculus
53	12	3.0	1238	11	Q8CIN9	Q8CIN9 mus musculus
54	12	3.0	1397	11	Q8CIN2	Q8CIN2 rattus norv
55	12	3.0	1406	13	Q9W6V5	Q9W6V5 gallus gall
56	12	3.0	1426	11	Q8CIN3	Q8CIN3 rattus norv
57	12	3.0	1461	5	O81GY3	O81GY3 drosophila
58	12	3.0	1462	5	Q9YU03	Q9YU03 drosophila
59	12	3.0	1705	11	Q9ERK5	Q9ERK5 mus musculus
60	11	2.7	157	4	Q8M470	Q8M470 homo sapien
61	11	2.7	198	5	Q23433	Q23433 caenorhabdi
62	11	2.7	207	13	Q9NL04	Q9NL04 eptaretus
63	11	2.7	253	13	Q9NL00	Q9NL00 eptaretus
64	11	2.7	306	13	O42243	O42243 xenopus lae
65	11	2.7	377	4	Q9UBT5	Q9UBT5 homo sapien
66	11	2.7	383	5	O8MTN0	O8MTN0 culicoides
67	11	2.7	398	11	Q82604	Q82604 rattus norv
68	11	2.7	405	4	Q9UBF0	Q9UBF0 homo sapien
69	11	2.7	405	6	Q29500	Q29500 oryctolagus
70	11	2.7	405	11	Q60998	Q60998 mus musculus
71	11	2.7	419	13	Q8Y1Q4	Q8Y1Q4 oryzias lat
72	11	2.7	433	6	Q8MTQ3	Q8MTQ3 aotus vocif
73	11	2.7	438	11	Q64642	Q64642 rattus norv
74	11	2.7	468	13	Q9NL06	Q9NL06 eptaretus
75	11	2.7	469	5	Q9NL14	Q9NL14 branchiost
76	11	2.7	470	5	Q9NL15	Q9NL15 branchiost
77	11	2.7	471	5	Q9Y1X6	Q9Y1X6 ephydatia f
78	11	2.7	471	13	Q91BA3	Q91BA3 potamotrygo
79	11	2.7	473	13	Q91B97	Q91B97 potamotrygo
80	11	2.7	473	13	Q9NL05	Q9NL05 eptaretus
81	11	2.7	478	5	Q9Y1X5	Q9Y1X5 ephydatia f
82	11	2.7	483	5	P91568	P91568 caenorhabdi
83	11	2.7	487	5	Q9NL13	Q9NL13 branchiost
84	11	2.7	488	5	Q9NL12	Q9NL12 branchiost
85	11	2.7	497	13	Q91B98	Q91B98 potamotrygo
86	11	2.7	505	13	Q91B96	Q91B96 potamotrygo
87	11	2.7	508	11	Q80W11	Q80W11 mus musculus
88	11	2.7	511	13	Q9NL07	Q9NL07 eptaretus
89	11	2.7	522	5	Q86AJ9	Q86AJ9 dictyosteli

90 11 2.7 536 4 Q8TE48 Q8te48 homo sapien  
 91 11 2.7 579 11 Q9J007 Q9j007 mus musculus  
 92 11 2.7 598 11 Q8BIW7 Q8biw7 mus musculus  
 93 11 2.7 642 11 Q60986 Q60986 mus musculus  
 94 11 2.7 649 11 Q64641 Q64641 rattus norv  
 95 11 2.7 659 11 Q63477 Q63477 rattus norv  
 96 11 2.7 699 11 Q61042 Q61042 mus musculus  
 97 11 2.7 793 4 Q7Z212 Q7z212 homo sapien  
 98 11 2.7 793 11 Q91V35 Q91v35 mus musculus  
 99 11 2.7 807 13 Q91969 Q91969 gallus gall  
 100 11 2.7 822 13 Q91556 Q91556 xenopus lae

## ALIGNMENTS

RESULT 1  
 OS5082 PRELIMINARY; PRT; 426 AA.  
 AC OS5082;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DE Protein-tyrosine-phosphatase (EC 3.1.3.48).  
 GN PTPN20.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=98070510; PubMed=9407093;  
 RA Ohnogi M., Kuranochi S., Matsuda S., Yamamoto T.;  
 RT "Molecular cloning and characterization of a novel cytoplasmic  
 RT protein-tyrosine phosphatase that is specifically expressed in  
 RT spermatocytes.";  
 RL J. Biol. Chem. 272:33092-33099(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; D64141; BA221761.1; .  
 DR EMBL; AK029493; BAC26476.1; .  
 DR HSSP; Q06124; 2SHP.  
 DR MGD; MGI:1196295; Ptpn20.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0004727; F:phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPPHTASE.  
 DR SMART; SM00194; PTEC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolyase.  
 SQ SEQUENCE 426 AA; 49118 MW; 2835FB3379502F4 CRC64;

Query Match 100.0%; Score 405; DB 11; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSSPRKVRGKTGNDNDEEGNSGNLRLNSLPSSSQKMTPTXPIFGNKNNSNVKPSHLL 60  
 DB 1 MSSPRKVRGKTGNDNDEEGNSGNLRLNSLPSSSQKMTPTXPIFGNKNNSNVKPSHLL 60

QY 61 SFSOKYELVYEPELESDDTDETVMDVSDRSLENRNNSMDSETAGSKTVSPVLSSSRLSK 120  
 DB 61 SFSOKYELVYEPELESDDTDETVMDVSDRSLENRNNSMDSETAGSKTVSPVLSSSRLSK 120  
 QY 121 DTEGVSSEKELTQIAQRPLIFNSSARSAMDCLNTLQKXELDIIRFLELEQMTLPDD 180  
 DB 121 DTEGVSSEKELTQIAQRPLIFNSSARSAMDCLNTLQKXELDIIRFLELEQMTLPDD 180  
 QY 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDVINASYIRIVNHHREYFIATQGPLPE 240  
 DB 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKDVINASYIRIVNHHREYFIATQGPLPE 240  
 QY 241 TIEDFWQVLNNCNVIAITREIECGVIKCYSWPISLKEPFEHFSVLETFHYTOY 300  
 DB 241 TIEDFWQVLNNCNVIAITREIECGVIKCYSWPISLKEPFEHFSVLETFHYTOY 300  
 QY 301 FTVRVFQIVKSGKSCVCHLQFTKWDHGTASADFFIKYVYVRKSHITGPLVHCS 360  
 DB 301 FTVRVFQIVKSGKSCVCHLQFTKWDHGTASADFFIKYVYVRKSHITGPLVHCS 360  
 QY 361 AGVGRGTGVFCVGVVPSAIEKNYSFDIMNIVTQMRKORCGMIQTK 405  
 DB 361 AGVGRGTGVFCVGVVPSAIEKNYSFDIMNIVTQMRKORCGMIQTK 405

## RESULT 2

Q9Y406 PRELIMINARY; PRT; 398 AA.  
 ID Q9Y406;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZP566K0524.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Ansgore W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL050040; CAB43248.1; .  
 DR PIR; T08716; T08716.  
 DR HSSP; Q06124; 2SHP.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPPHTASE.  
 DR SMART; SM00194; PTEC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hypothetical protein; Hydrolase.  
 FT NON TER 1  
 SQ SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;

Query Match 4.7%; Score 19; DB 4; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210  
 DB 164 KNYRDILPYDSTRVPLGK 182  
 RESULT 3  
 Q9QWQ7 PRELIMINARY; PRT; 336 AA.  
 ID Q9QWQ7

AC Q9QW07;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PTP-RL10b.  
 GN PTPN21.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57-Bl6; TISSUE=Testis;  
 RA Nishiyama H., Hicashitsuiji H., Fujita J.;  
 RT "Expression of mouse PTP-RL10 isoforms in testis."  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; D83072; BAA19740.1; -;  
 DR HSSP; P29350; IGW2.  
 DR MGD; MGI:134406; Ptpn21.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PTPPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.  
 SQ SEQUENCE 336 AA; 38503 MW; 679B683660C39FFD CRC64;

Query Match 3.7%; Score 15; DB 11; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCAGVGRGTG 368  
 DB 265 PLLVHCAGVGRGTG 279  
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RESULT 4  
 Q9Y1X4 PRELIMINARY; PRT; 446 AA.  
 AC Q9Y1X4;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE SPTPR5 (Fragment).  
 OS Ephydatia fluviatilis.  
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;  
 OC Aploosclerida; Spongillidae; Ephydatia.  
 OX NCBI\_TaxID=31330;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99246376; PubMed=10229569;  
 RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;  
 RT "Multiple protein tyrosine phosphatases in sponges and explosive gene  
 duplication in the early evolution of animals before the parazoan-  
 eumetazoan split."  
 RL J. Mol. Evol. 48:654-662(1999).  
 DR EMBL; AB039127; BAA82560.1; -;  
 DR HSSP; F18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PTPPHPTASE.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON TER 1  
 SQ SEQUENCE 446 AA; 50365 MW; 9B5B8AF6168FDF7C CRC64;

Query Match 3.7%; Score 15; DB 5; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 GPLLVHCAGVGRGTG 367  
 DB 102 GPLLVHCAGVGRGTG 116  
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RESULT 5  
 Q7TWG1 PRELIMINARY; PRT; 758 AA.  
 ID Q7TWG1;  
 AC Q7TWG1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protein tyrosine phosphatase, non-receptor type 21 (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udwin T.B., Toshynski S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Breast tumor;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; BC055942; AAH55942.1; -;  
 KW Receptor.  
 FT NON TER 1  
 SQ SEQUENCE 758 AA; 85514 MW; 6C3CAB40C026BD37 CRC64;

Query Match 3.7%; Score 15; DB 11; Length 758;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCAGVGRGTG 368  
 DB 687 PLLVHCAGVGRGTG 701  
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RESULT 6  
 Q8WX29 PRELIMINARY; PRT; 1024 AA.  
 ID Q8WX29





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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
RL Nature 420:563-573 (2002).
DR EXBL: AK034067; BAC28569.1; -.
DR MGD; MGI:97812; Fcprd.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR Phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00404; PTPC_motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
FT NON TER 1
SQ SEQUENCE 79 AA; 8970 MW; EA7CAE6839241155 CRC64;

Query Match 3.5%; Score 14; DB 11; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370
DB 9 VHCAGVGRGTGVFI 22

RESULT 10
Q8CC54 PRELIMINARY; PRT; 93 AA.
AC Q8CC54;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Unknown EST (Fragment).
GN FIPRD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
RL Nature 420:563-573 (2002).
DR EXBL: AK033873; BAC28503.1; -.
DR MGD; MGI:97812; Fcprd.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR Phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00404; PTPC_motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
FT NON TER 1
SQ SEQUENCE 93 AA; 10642 MW; 1BCCF472432BA0CD CRC64;

Query Match 3.5%; Score 14; DB 11; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370
DB 23 VHCAGVGRGTGVFI 36

RESULT 11
Q9UM23 PRELIMINARY; PRT; 134 AA.
AC Q9UM23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase RQ (Fragment).
GN PTP-RO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Dayton M.A., Blanchard K.L.;
RT "Differential expression of PTPase RNAs resulting from K562
RT differentiation induced by PMA."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169351; AAD50277.1; -.
DR HSP; P18052; LYFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT NON TER 1
FT NON TER 134
SQ SEQUENCE 134 AA; 15344 MW; 6E848021FC54368C CRC64;

Query Match 3.5%; Score 14; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370
DB 99 VHCAGVGRGTGVFI 112

RESULT 12
Q9YIX3 PRELIMINARY; PRT; 183 AA.
AC Q9YIX3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SPTP3 (Fragment).
OS Ephydatia fluviatilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Spongillidae; Ephydatia.
OX NCBI_TaxID=31330;
RN [1]_TaxID=31330;
RP SEQUENCE FROM N.A.
RX MEDLINE=99246376; PubMed=10229569;
RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;
RT "Multiple protein tyrosine phosphatases in sponges and explosive gene
RT duplication in the early evolution of animals before the parazoan-
RT emetazoan split."
RL J. Mol. Evol. 48:654-662 (1999).

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DR EMBL; AB019128; BAA82561.1; --  
 DR HSSP; P18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPPHTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.  
 FT NON\_TER  
 SQ SEQUENCE 183 AA; 20507 MW; AECDBFF661EDBEC CRC64;  
 [1]  
 Query Match 3.5%; Score 14; DB 5; Length 183;  
 Best Local Similarity 100.0%; Pred.No.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 354 PLLVHCSAGVGRGTG 367  
 DB 109 PLLVHCSAGVGRGTG 122

RESULT 13  
 QBC922 PRELIMINARY; PRT; 192 AA.  
 AC QBC922;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Unknown EST (Fragment).  
 GN PTPRD.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The RIKEN Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK043201; BAC31488.1; --  
 DR MGD; MGI:97812; Ptpd  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003595; PTPC motif.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPPHTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR SMART; SM00404; PTPC motif; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 FT NON\_TER  
 SQ SEQUENCE 192 AA; 22551 MW; B78B194500F33B1A CRC64;

Query Match 3.5%; Score 14; DB 11; Length 192;  
 Best Local Similarity 100.0%; Pred.No.3.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGRGTGVFI 370  
 DB 122 VHCSAGVGRGTGVFI 135

RESULT 14  
 Q62917 PRELIMINARY; PRT; 460 AA.  
 AC Q62917;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE IAR receptor-linked tyrosine phosphatase.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague Dawley; TISSUE=Brain;  
 RX MEDLINE=94075340; PubMed=8253779;  
 RA Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,  
 RA Brosius J.,  
 RA "Leukocyte common antigen-related receptor-linked tyrosine  
 RT phosphatase. Regulation of mRNA expression."  
 RL J. Biol. Chem. 268:26503-26511(1993).  
 DR EMBL; U00477; AAC04306.1; --  
 DR PIR; A56493; A56493.  
 DR HSSP; P18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PS00700; PRTYPPHTASE.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Receptor.  
 SQ SEQUENCE 460 AA; 52989 MW; B78C8E504F1260FA CRC64;

Query Match 3.5%; Score 14; DB 11; Length 460;  
 Best Local Similarity 100.0%; Pred.No.7e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGRGTGVFI 370  
 DB 390 VHCSAGVGRGTGVFI 403

RESULT 15  
 Q91BA5 PRELIMINARY; PRT; 468 AA.  
 AC Q91BA5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE RYTPR2Aa protein (fragment).  
 GN RYTPR2Aa.  
 OS Potamotrygon motoro (South American freshwater stingray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hypnosqualea; Pristigasteria; Batoidae;  
 OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.  
 CX NCBI\_TaxID=86373;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20219325; PubMed=10754074;  
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RA "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;  
 RT divergence of tissue-specific isoform genes in the early evolution of  
 RT vertebrates."  
 RL J. Mol. Evol. 50:302-311(2000).  
 DR EMBL; AB033581; BAA95188.1; --  
 DR HSSP; P18052; IYFO.

DR GO:0016787; F:hydrolase activity; IEA.  
 DR GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON\_TER

SEQUENCE 468 AA; 53862 MW; 0051F5B0EDD7A580 CRC64;  
 Query Match 3.5%; Score 14; DB 13; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTGVFI 370  
 DB 398 VHCAGVGRTGVFI 411  
 |||||

## RESULT 16

Q91BA2 PRELIMINARY; PRT; 468 AA.  
 AC Q91BA2  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RYPTPR2AB protein (Fragment).  
 GN RYPTPR2AB.  
 OS Potamotrygon motoro (South American freshwater stingray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hyposqualea; Pristiorajae; Batoidae;  
 OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.  
 OX NCBI\_TaxID=86373;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20219325; PubMed=10754074;  
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 FT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;  
 divergence of tissue-specific isoform genes in the early evolution of  
 vertebrates.";  
 RL J. Mol. Evol. 50:302-311(2000).  
 DR EMBL; AB033584; BAA95191.1; -;  
 DR HSSP; P18052; IYFO.  
 DR GO:0016787; F:hydrolase activity; IEA.  
 DR GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON\_TER

SEQUENCE 468 AA; 53862 MW; 8B1CABE0EE9692E4 CRC64;  
 Query Match 3.5%; Score 14; DB 13; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTGVFI 370  
 DB 398 VHCAGVGRTGVFI 411  
 |||||

## RESULT 17

Q91BA0 PRELIMINARY; PRT; 468 AA.  
 AC Q91BA0  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RYPTPR2AC protein (Fragment).  
 GN RYPTPR2AC.  
 OS Potamotrygon motoro (South American freshwater stingray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hyposqualea; Pristiorajae; Batoidae;  
 OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.  
 OX NCBI\_TaxID=86373;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20219325; PubMed=10754074;  
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 FT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;  
 divergence of tissue-specific isoform genes in the early evolution of  
 vertebrates.";  
 RL J. Mol. Evol. 50:302-311(2000).  
 DR EMBL; AB033586; BAA95193.1; -;  
 DR HSSP; P18052; IYFO.  
 DR GO:0016787; F:hydrolase activity; IEA.  
 DR GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON\_TER

SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;  
 Query Match 3.5%; Score 14; DB 13; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTGVFI 370  
 DB 398 VHCAGVGRTGVFI 411  
 |||||

## RESULT 18

Q90VJ5 PRELIMINARY; PRT; 508 AA.  
 AC Q90VJ5  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Receptor protein-tyrosine phosphatase LAR (fragment).  
 GN PTPR OR LAR.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van der Sar A., Betist M., de Fockert J., Overvoorde J., Zivkovic D.,  
 RA den Hertog J.;  
 FT "Expression of receptor protein-tyrosine phosphatase alpha, sigma and  
 LAR during development of the zebrafish embryo.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ311885; CAC44758.1; -;  
 DR ZFIN; ZDB-GENE-020107-2; ptpri.  
 DR GO:0016787; F:hydrolase activity; IEA.  
 DR GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO:0006470; P:protein amino acid dephosphorylation; IEA.

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DR InterPro: IPR000387; TYR phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PR00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 2.
DR KW Hydrolase.
DR FT NON_TER
DR SQ SEQUENCE 508 AA; 58463 MW; 72A6DD348830C446 CRC64;

Query Match 3.5%; Score 14; DB 13; Length 508;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTGVPI 370
DB 438 VHCAGVGRTGVPI 451

RESULT 19
Q64696
ID Q64696 PRELIMINARY; PRT; 582 AA.
AC Q64696;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein-tyrosine phosphatase, receptor-type, P polypeptide
DE (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related) (Fragment).
DE PTERF OR LAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE=95394448; PubMed=7665159;
RA Schaapveld R.O.J., Van den Maagdenberg A.M.J.M., Schepens J.T.G.,
RA Weghuis D.O., van Kessel A.G., Wieringa B., Hendriks W.J.A.J.;
RT "The mouse gene Ptpfr encoding the leukocyte common antigen-related
RT molecule LAR: cloning, characterization, and chromosomal
RT localization.";
RL Genomics 27:124-130(1995).
RN [2]
RN SEQUENCE OF 116-221 AND 405-512 FROM N.A.
RP STRAIN=BALB/C; TISSUE=BRAIN;
RC MEDLINE=95394448; PubMed=7832766;
RX Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RA "A novel receptor-type protein tyrosine phosphatase with a single
RA catalytic domain is specifically expressed in mouse brain.";
RT Biochem. J. 305:499-504(1995)
RL Mol. Biol. Rep. 16:241-248(1992).
RN [3]
RN SEQUENCE OF 116-221 FROM N.A.
RP STRAIN=BALB/C; TISSUE=BRAIN;
RC MEDLINE=95134322; PubMed=7832766;
RX Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RA "A novel receptor-type protein tyrosine phosphatase with a single
RA catalytic domain is specifically expressed in mouse brain.";
RT Biochem. J. 305:499-504(1995)
RL Mol. Biol. Rep. 16:241-248(1992).
RN [3]
CC -!- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR. IT
CC POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
CC (PTPASE) (BY SIMILARITY).
CC -!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC THE FIRST ONE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-LIKE
CC DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A
CC CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.

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CC -!- SIMILARITY: TO DPTP AND TO LAR.
DR EMBL: Z37988; CAA86070.1; -.
DR EMBL: Z23061; CAA80596.1; -.
DR EMBL: Z23049; CAA80584.1; -.
DR PIR: A57068; A57068.
DR HGSP: P18052; LYFO.
DR MGD: MGI:103695; Ptpfr.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005194; F: cell adhesion molecule activity; IEA.
DR GO: GO:0016787; F: hydrolase activity; IEA.
DR GO: GO:0004727; F: prenylated protein tyrosine phosphatase act. .; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0007155; P: cell adhesion; IEA.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR InterPro: IPR000387; TYR phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 2.
DR KW Hydrolase; Receptor; Glycoprotein; Transmembrane; Cell adhesion;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN <1 582 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 291 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 334 582 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 223 223 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
FT SQ SEQUENCE 582 AA; 66965 MW; 933C3C08536342FE CRC64;

Query Match 3.5%; Score 14; DB 11; Length 582;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTGVPI 370
DB 512 VHCAGVGRTGVPI 525

RESULT 20
Q9IA18
ID Q9IA18 PRELIMINARY; PRT; 615 AA.
AC Q9IA18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20193505; PubMed=10727868;
RX Johnson K.G., Holt C.E.;
RA "Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the
RA developing xenopus visual system.";
RT Mech. Dev. 92:291-294(2000).
RL EMBL: AF198450; AAF43607.1; -.
DR HGSP: P18052; LYFO.
DR GO: GO:0016787; F: hydrolase activity; IEA.
DR GO: GO:0004727; F: protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR InterPro: IPR000387; TYR phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 2.

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DR PROSITE; PS50055; TVR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
FT NON\_TER 1 1  
SQ SEQUENCE 615 AA; 70728 MW; 42593554887858AC CRC64;  
  
Query Match 3.5%; Score 14; DB 13; Length 615;  
Best Local Similarity 100.0%; Pred. No. 9.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 357 VHCSAGVGRGTGVFI 370  
Db 545 VHCSAGVGRGTGVFI 559  
|||||  
RESULT 21  
Q8R169 PRELIMINARY; PRT; 749 AA.  
AC Q8R169;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
CS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; SC025145; AAH25145.1; -.  
DR PIR; S40282; S40282.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_PTP.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
DR PROSITE; PS50056; TVR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS50055; TVR\_PHOSPHATASE\_PTP; 2.  
KW Hypothetical protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 749 AA; 86082 MW; 421PC68950C959E CRC64;  
  
Query Match 3.5%; Score 14; DB 11; Length 749;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 357 VHCSAGVGRGTGVFI 370  
Db 679 VHCSAGVGRGTGVFI 692  
|||||  
RESULT 22  
Q90YJ4 PRELIMINARY; PRT; 857 AA.  
AC Q90YJ4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Receptor protein-tyrosine phosphatase sigma (fragment).  
GN PTPRS OR RPTPSIGMA.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
CX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC van der Sar A., Betist M., de Fockert J., Overvoorde J., Zivkovic D.,

den Hertog J.;  
RT "Expression of receptor protein-tyrosine phosphatase alpha, sigma and  
LAR during development of the zebrafish embryo."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ311886; CAC44759.1; -.  
DR ZFIN; ZDB-GENE-020107-3; ptpre.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
DR PROSITE; PS50056; TVR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS50055; TVR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
FT NON\_TER 1 1  
SQ SEQUENCE 857 AA; 97709 MW; 604A926BB08B81D8 CRC64;  
  
Query Match 3.5%; Score 14; DB 13; Length 857;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 357 VHCSAGVGRGTGVFI 370  
Db 787 VHCSAGVGRGTGVFI 800  
|||||  
RESULT 23  
Q723X4 PRELIMINARY; PRT; 1191 AA.  
ID Q723X4;  
AC Q723X4;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686B1310 (Fragment).  
GN DKFZP686B1310  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human cervix;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX537361; CAD97607.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 1191 AA; 134914 MW; 8320FEED0ADAC278 CRC64;  
  
Query Match 3.5%; Score 14; DB 4; Length 1191;  
Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 357 VHCSAGVGRGTGVFI 370  
Db 1121 VHCSAGVGRGTGVFI 1134  
|||||  
RESULT 24  
Q17024 PRELIMINARY; PRT; 1231 AA.  
ID Q17024;  
AC Q17024;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Anlar protein (Fragment).  
GN ANLAR.

OS Anopheles gambiae (African malaria mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
 OX NCBI\_TaxID=7165;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=KWA;  
 RT Spiera S.;  
 RA "Anlar-a transmembrane, receptor-like protein tyrosine phosphatase  
 from the mosquito, Anopheles gambiae.";  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X85217; CAA59483.1; -;  
 DR PIR; S53089; S53089.  
 DR HSSP; P18052; 1YFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003961; FN.III.  
 DR InterPro; IPR008957; FN.III-like.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR InterPro; IPR00041; FN3; 4.  
 DR Pfam; PF00041; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 2.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON TER  
 SQ SEQUENCE 1231 AA; 140463 MW; 53A1149338B5AAC3 CRC64;  
 Query Match 3.5%; Score 14; DB 5; Length 1231;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGTGVFI 370  
 DB 1161 VHCAGVGRGTGVFI 1174  
 RESULT 25  
 Q8VEV0  
 ID Q8VEV0 PRELIMINARY; PRT; 1254 AA.  
 AC Q8VEV0;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protein tyrosine phosphatase, receptor type, delta A.  
 GN PTPRD.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=DR/23, and C57BL/6J; TISSUE=Brain;  
 RA Fehr C., Belknap J.K., Crabbe J.C., Buck K.J.;  
 RT "High resolution mapping of a quantitative trait locus for acute  
 ethanol withdrawal on mouse chromosome 4 and characterization of  
 potential candidate genes.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF326560; AAL37406.1; -;  
 DR EMBL; AF326559; AAL37405.1; -;  
 DR PIR; S40282; S40282.  
 DR MGD; MGI:197812; Ptpd.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003962; FN.III.  
 DR InterPro; IPR003961; FN.III.

DR InterPro; IPR008957; FN.III-like.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; FN3; 3.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS0635; IG-LIKE; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Receptor; Repeat.  
 SQ SEQUENCE 1254 AA; 141639 MW; 95EF17485C61CBF6 CRC64;  
 Query Match 3.5%; Score 14; DB 11; Length 1254;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGTGVFI 370  
 DB 1184 VHCAGVGRGTGVFI 1197  
 RESULT 26  
 Q75870  
 ID Q75870 PRELIMINARY; PRT; 1399 AA.  
 AC Q75870;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE PTPalpha (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
 Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,  
 RA Danganan L., Exler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
 RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC005788; AAC62834.1; -;  
 DR HSSP; P18052; 1YFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003962; FN.III subd.  
 DR InterPro; IPR003961; FN.III.  
 DR InterPro; IPR008957; FN.III-like.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; FN3; 6.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 5.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Repeat.

FT NON TER 1 1  
 FT NON TER 1399 1399  
 SQ SEQUENCE 1399 AA; 157055 MW; EEOA8CC9FD83C7C1 CRC64;

Query Match 3.5%; Score 14; DB 4; Length 1399;  
 Best Local Similarity 100.0%; Pred. No. 2.e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTGVFI 370  
 |||||  
 Db 1351 VHCAGVGRGTGVFI 1364

## RESULT 27

Q90815  
 ID Q90815 PRELIMINARY; PRT; 1499 AA.  
 AC Q90815;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protein-tyrosine phosphatase.  
 GN CYPALPHA1.  
 OS Gallus Gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95001563; PubMed=7918104;  
 RA Stoker A.W.;  
 RT "Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase are implicated in neural development."  
 RL Mech. Dev. 46:201-217(1994).  
 RL ENBL; L32780; AA464460.1; -.  
 DR PIR; I50212; I50212.  
 DR HSP; P18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003387; TYR phosphatase.  
 DR Pfam; PF00041; fn3; 4.  
 DR Pfam; PF00047; ig; 3.  
 DR PRINTS; PR00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00114; FNTYPEIII.  
 DR SMART; SM00700; PRTYPHPHTASE.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 1499 AA; 168570 MW; ALFBD6E3C2453F82 CRC64;

Query Match 3.5%; Score 14; DB 13; Length 1499;  
 Best Local Similarity 100.0%; Pred. No. 2.e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTGVFI 370  
 |||||  
 Db 1430 VHCAGVGRGTGVFI 1443

## RESULT 28

Q90W00  
 ID Q90W00 PRELIMINARY; PRT; 1501 AA.  
 AC Q90W00;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Receptor protein tyrosine phosphatase-sigma, RPTP-sigma.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94043351; PubMed=8227050;  
 RA Yan H., Grossman A., Wang H., D'Eustachio P., Mossie K., Musacchio J.M., Silvennoinen O., Schlesinger J.;  
 RT "A novel receptor tyrosine phosphatase-sigma that is highly expressed in the nervous system."  
 RL J. Biol. Chem. 268:24880-24886(1993).  
 DR HSP; P18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 4.  
 DR Pfam; PF00047; ig; 3.  
 DR PRINTS; PR00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00114; FNTYPEIII.  
 DR SMART; SM00700; PRTYPHPHTASE.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 1501 AA; 168336 MW; C3E0889B4BEP430D CRC64;

Query Match 3.5%; Score 14; DB 11; Length 1501;  
 Best Local Similarity 100.0%; Pred. No. 2.e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTGVFI 370  
 |||||  
 Db 1431 VHCAGVGRGTGVFI 1444

## RESULT 29

Q7TT17  
 ID Q7TT17 PRELIMINARY; PRT; 1501 AA.  
 AC Q7TT17;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Query Match 3.5%; Score 14; DB 13; Length 1499;  
 Best Local Similarity 100.0%; Pred. No. 2.e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTGVFI 370  
 |||||  
 Db 1430 VHCAGVGRGTGVFI 1443

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Kuzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT -generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16898-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.,  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC052462; AAH52462.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 1501 AA; 168297 MW; 444381DDFE83BF41 CRC64;  
  
Query Match 3.5%; Score 14; DB 11; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 357 VHCAGVGRGTGVFI 370  
Db 1431 VHCAGVGRGTGVFI 1444  
|||||  
  
RESULT 30  
Q9UM81 PRELIMINARY; PRT; 1502 AA.  
AC Q9UM81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE PTPsigma-(brain) precursor.  
GN PTPSIGMA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Endo N., Rutledge S.J., Opas B.E., Vogel R., Rodan G.A., Schmidt A.,  
RT "Human protein tyrosine phosphatase-sigma: Alternative splicing and  
RT inhibition by biophosphates.";  
RL J. Bone Miner. Res. 0:0-0(1995).  
DR EMBL: U41725; AAD09360.1; -  
DR HSSP; P18052; IYFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG c2.  
DR InterPro; IPR000387; TYR phosphatase.  
DR Pfam; PF00041; fn3; 4.  
DR Pfam; PF00047; ig; 3.  
DR PRINTS; PR00014; ENTPEIII.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 4.  
DR SMART; SM00408; IGC2; 2.  
  
Query Match 3.5%; Score 14; DB 11; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 357 VHCAGVGRGTGVFI 370  
Db 1431 VHCAGVGRGTGVFI 1444  
|||||  
  
RESULT 30  
Q9UM81 PRELIMINARY; PRT; 1502 AA.  
AC Q9UM81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE PTPsigma-(brain) precursor.  
GN PTPSIGMA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Endo N., Rutledge S.J., Opas B.E., Vogel R., Rodan G.A., Schmidt A.,  
RT "Human protein tyrosine phosphatase-sigma: Alternative splicing and  
RT inhibition by biophosphates.";  
RL J. Bone Miner. Res. 0:0-0(1995).  
DR EMBL: U41725; AAD09360.1; -  
DR HSSP; P18052; IYFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG c2.  
DR InterPro; IPR000387; TYR phosphatase.  
DR Pfam; PF00041; fn3; 4.  
DR Pfam; PF00047; ig; 3.  
DR PRINTS; PR00014; ENTPEIII.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 4.  
DR SMART; SM00408; IGC2; 2.

DR SMART; SM00194; PTPc; 2.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00566; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase; Immunoglobulin domain; Signal.  
FT SIGNAL 1 28 POTENTIAL.  
SQ SEQUENCE 1502 AA; 168788 MW; AD6705AFEB0F3CFD CRC64;  
  
Query Match 3.5%; Score 14; DB 4; Length 1502;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 357 VHCAGVGRGTGVFI 370  
Db 1432 VHCAGVGRGTGVFI 1445  
|||||  
  
RESULT 31  
Q9IAJ0 PRELIMINARY; PRT; 1788 AA.  
ID Q9IAJ0;  
AC Q9IAJ0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Receptor protein tyrosine phosphatase LAR.  
GN XPTP-LAR.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20193505; PubMed=10727868;  
RA Johnson K.G., Holt C.E.;  
RT "Expression of CrYP-alpha, LAR, PTP-delta, and PTP-rho in the  
RT developing xenopus visual system.";  
RL Mech. Dev. 92:291-294(2000).  
DR EMBL; AF197945; AAF43606.1; -  
DR HSSP; P18052; IYFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG c2.  
DR InterPro; IPR000387; TYR phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 7.  
DR Pfam; PF00047; ig; 3.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR SMART; SM00060; FN3; 7.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00194; PTPc; 2.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00566; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase; Immunoglobulin domain; Repeat.  
SQ SEQUENCE 1788 AA; 200271 MW; AB192549866D9067 CRC64;  
  
Query Match 3.5%; Score 14; DB 13; Length 1788;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 357 VHCAGVGRGTGVFI 370  
Db 1718 VHCAGVGRGTGVFI 1731  
|||||  
  
RESULT 32



Q64605 Q64605 PRELIMINARY; PRT; 1863 AA.  
AC Q64605; Q64675; Q07808; Q64621;  
DT 01-NOV-1996 (TRENDELREL 01, Created)  
DT 01-NOV-1996 (TRENDELREL 01, Last sequence update)  
DT 01-OCT-2003 (TRENDELREL 25, Last annotation update)  
DE Leukocyte common antigen-related phosphatase ptp2 precursor  
DE (EC 3.1.3.48) (Protein-tyrosine phosphatase LAR-PTP2) (phosphotyrosine  
DE phosphatase LAR-PTP2) (PTase LAR-PTP2) (PTP NE-3) (ZTP-P1) (CPTP1)  
DE (PTP-sigma). 3N LAR-PTP2.  
CS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS LAR-PTP2 AND LAR-PTP2B).  
RC STRAIN=Sprague-Dawley; TISSUE=Liver, and Brain;  
RX MEDLINE=94347119; PubMed=8068021;  
RA Zhang W.R., Hashimoto N., Ahmad F., Ding W., Goldstein B.J.,  
RT "Molecular cloning and expression of a unique receptor-like protein-  
RT tyrosine-phosphatase in the leucocyte-common-antigen-related phosphate  
RT family.";  
RL Biochem. J. 302:39-47(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM LAR-PTP2B).  
RC TISSUE=Brain cortex;  
RX MEDLINE=93357030; PubMed=8352946;  
RA Walton K.M., Martelli K.J., Kwak S.P., Dixon J.E., Largent B.L.;  
RT "A novel receptor-type protein tyrosine phosphatase is expressed  
RT during neurogenesis in the olfactory neuroepithelium.";  
RL Neuron 11:387-400(1993).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS PTP-P1 AND PTP-PS).  
RC TISSUE=Phaeochromocytoma;  
RX MEDLINE=93374907; PubMed=8396131;  
RA Pan M.-G., Rim C., Lu K.P., Florio T., Stork P.J.S.;  
RT "Cloning and expression of two structurally distinct receptor-linked  
RT protein-tyrosine phosphatases generated by RNA processing from a  
RT single gene.";  
RL J. Biol. Chem. 268:19284-19291(1993).  
CC -!- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR. IT  
CC POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY  
CC (PTPASE) (BY SIMILARITY).  
CC -!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMOLOGICAL ACTIVITY, WHILE  
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE  
CC FIRST ONE (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATASE + H(2)O = PROTEIN  
CC TYROSINE + ORTHOPHOSPHATE.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Comment=Additional isoforms seem to exist;  
CC Name=LAR-PTP2;  
CC IsoId=Q64605-1; Sequence=Displayed;  
CC Name=LAR-PTP2B;  
CC IsoId=Q64605-2; Sequence=VSP\_050356, VSP\_050357;  
CC Name=PTP-P1;  
CC IsoId=Q64605-3; Sequence=VSP\_050356, VSP\_050357;  
CC Name=PTP-PS;  
CC IsoId=Q64605-4; Sequence=VSP\_050356, VSP\_050357, VSP\_050358,  
CC VSP\_050359;  
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN HEART, TESTIS AND LIVER, AND  
CC IN A LESSER EXTENT IN SKELETAL MUSCLE, SPLEEN, BRAIN AND KIDNEY.  
CC EXPRESSED SELECTIVELY IN BOTH BRAIN AND OLFACTORY NEUROEPITHELIUM.  
CC IN BRAIN IT IS EXPRESSED AT HIGH LEVELS IN THE PYRAMIDAL CELLS OF  
CC THE HIPPOCAMPUS AND AT LOWER LEVELS IN THE THALAMUS, CEREBRAL  
CC CORTEX, AND CEREBELLUM.  
CC -!- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
CC EMBL; L11587; AAC37656.1; -;  
CC EMBL; L12329; AAC37657.1; -;

DR EMBL; L19333; AAA42309.1; -;  
DR EMBL; L19180; AAA75407.1; -;  
DR EMBL; L19181; AAA50568.1; -;  
DR HSP; P18052; LYPO.  
DR GO; GO:0016021; C.integral to membrane; IEA.  
DR GO; GO:0005194; F.cell adhesion molecule activity; IEA.  
DR GO; GO:0016787; F.hydrolase activity; IEA.  
DR GO; GO:0004772; F.phosphatase activity; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR GO; GO:0007155; F.cell adhesion; IEA.  
DR GO; GO:0006470; P.protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN-III-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR000387; TYR phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00041; fn3; 7.  
DR Pfam; PF00047; ig; 3.  
DR Pfam; PF00102; Y.phosphatase; 2.  
DR PRINTS; PR00014; ENTPEELI.  
DR PRINTS; PR00700; PRTYPEPTASE.  
DR SMART; SM00060; FN3; 7.  
DR SMART; SM00408; IGc2; 3.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
KW Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
FT CHAIN 1 26  
FT SIGNAL  
FT CHAIN 27 1863  
FT LEUCOCYTE COMMON ANTIGEN-RELATED  
FT PHOSPHATASE PTP2.  
FT EXTRACELLULAR (POTENTIAL).  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT IG-LIKE C2-TYPE DOMAIN 1.  
FT IG-LIKE C2-TYPE DOMAIN 2.  
FT IG-LIKE C2-TYPE DOMAIN 3.  
FT IG-LIKE C2-TYPE DOMAIN 4.  
FT PROTEIN-TYROSINE PHOSPHATASE 1.  
FT PROTEIN-TYROSINE PHOSPHATASE 2.  
FT POLY-ALA.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT POTENTIAL.  
FT POTENTIAL.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT Missing (in isoform LAR-PTP2B, isoform  
FT PTP-P1 and isoform PTP-PS).  
FT /FTID=VSP\_050356.  
FT V -> I (in isoform LAR-PTP2B, isoform  
FT PTP-P1 and isoform PTP-PS).  
FT /FTID=VSP\_050357.  
FT KLASKAHTSRPTASLPCKNFKRL -> VTAGPQWTGGL  
FT KTDHSCQLPTHTQ (in isoform PTP-PS).  
FT /FTID=VSP\_050358.  
FT Missing (in isoform PTP-PS).  
FT /FTID=VSP\_050359.  
FT NS -> KQ (IN REF. 3; AAA75407 AND  
FT AAA50568).  
FT T -> P (IN REF. 3; AAA75407 AND  
FT AAA50568).  
FT Q -> D (IN REF. 3; AAA75407 AND  
FT AAA50568).  
FT S -> A (IN REF. 3; AAA75407 AND  
FT AAA50568).  
FT

FT CONFLICT 352 369 IEYKSDQDPVQIKEDI -> LSIKARMGRHSKTS  
(IN REF. 3; AAA75407 AND AAA50568).  
FT CONFLICT 398 400 GPP -> AP (IN REF. 3; AAA75407 AND  
AAA50568).  
FT CONFLICT 597 597 C -> R (IN REF. 3; AAA75407 AND  
AAA50568).  
FT CONFLICT 1105 1105 G -> P (IN REF. 3; AAA75407 AND  
AAA50568).  
FT CONFLICT 1124 1125 RR -> S (IN REF. 3; AAA75407 AND  
AAA50568).  
FT CONFLICT 1604 1613 SSKAHTSRPI -> APRHLRDSF (IN REF. 3;  
AAA75407).  
FT CONFLICT 1732 1732 Q -> E (IN REF. 3; AAA75407).  
FT CONFLICT 1756 1756 MISSING (IN REF. 3; AAA75407).  
FT CONFLICT 1854 1854 MISSING (IN REF. 3; AAA75407).  
SQ SEQUENCE 1863 AA; 207011 MW; E2D5D2612EFCF7AA CRC64;  
Query Match 3.5%; Score 14; DB 11; Length 1863;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 357 VHCAGVGRGTGVP 370  
Db 1793 VHCAGVGRGTGVP 1806  
RESULT 33  
Q9QW67 PRELIMINARY; PRT; 1887 AA.  
AC Q9QW67;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE LAR, leukocyte common antigen-related PROTEIN-TRANSMEMBRANE receptor  
phosphotyrosine phosphatase.  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92278755; PubMed=1317540;  
RA Xu Q., Lenardo T., Weinberg R.A.;  
RT "The N-terminal and C-terminal domains of a receptor tyrosine  
phosphatase are associated by non-covalent linkage.";  
RL Oncogene 7:1051-1057(1992).  
DR HSP; P18052; IYFO.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR GO: GO:0016787; F:hydrolase activity; IEA.  
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig-c2.  
DR InterPro; IPR001005; Myb DNA binding.  
DR InterPro; IPR000387; Tyr phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 7.  
DR Pfam; PF00047; ig; 3.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00014; FNTYPEII.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00408; IGC2; 2.  
DR SMART; SM00194; STPC; 2.  
DR PROSITE; PS50835; IG\_LIK3; 3.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.

KW Hydrolase; Immunoglobulin domain; Repeat.  
SQ SEQUENCE 1887 AA; 210453 MW; B84B33E7E4E70281 CRC64;  
Query Match 3.5%; Score 14; DB 11; Length 1887;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 357 VHCAGVGRGTGVP 370  
Db 1817 VHCAGVGRGTGVP 1830  
RESULT 34  
Q64487 PRELIMINARY; PRT; 1894 AA.  
AC Q64487; Q64486; Q64488; Q64495;  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Protein-tyrosine phosphatase, receptor-type, D precursor (EC 3.1.3.48)  
DE (Protein-tyrosine phosphatase delta) (R-PTP-delta).  
GN PTPRD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C; TISSUE=BRAIN;  
RX MEDLINE=93360986; PubMed=8355697;  
RA Mizuno K., Hasegawa K., Katagiri T., Ogimoto M., Ichikawa T.,  
RA Yakura H.;  
RT "MPTP delta, a putative murine homolog of HPTP delta, is expressed in  
specialized regions of the brain and in the B-cell lineage.";  
RL Mol. Cell. Biol. 13:5513-5523(1993).  
RN [2]  
RP SEQUENCE OF 1430-1534 FROM N.A.  
RC STRAIN=BA1B/C; TISSUE=BRAIN;  
RX MEDLINE=95134232; PubMed=7832766;  
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;  
RT "A novel receptor-type protein tyrosine phosphatase with a single  
catalytic domain is specifically expressed in mouse brain.";  
RL Biochem. J. 305:499-504(1995).  
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN  
TYROSINE + PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS.  
CC Event-Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=C;  
CC Name=A;  
CC IsoId=Q64487-1; Sequence=Displayed;  
CC IsoId=Q64487-2; Sequence=VSP\_050406, VSP\_050407, VSP\_050408;  
CC Name=B;  
CC IsoId=Q64487-3; Sequence=VSP\_050406, VSP\_050407;  
CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, HEART, AND SOME B-CELL LINES.  
CC -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN  
FROM THE TRANSMEMBRANE SEGMENT (BY SIMILARITY).  
CC -1- SIMILARITY: EXTRACELLULAR REGION TYPICAL OF A CAM FAMILY (3 IG-  
LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND  
A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.  
EMBL; D13903; BAA03003.1; -;  
EMBL; D13905; BAA03005.1; -;  
EMBL; D13904; BAA03004.1; -;  
EMBL; Z23051; CAA80586.1; -;  
PIR; C54689; CS4689.  
HSP; P18052; IYFO.  
MGD; MGI:97812; Ptpcd.  
GO; GO:0016021; C:integral to membrane; IEA.  
GO; GO:0016787; F:hydrolase activity; IEA.  
GO; GO:0004727; F:phosphorylated protein tyrosine phosphatase act.; IEA.  
GO; GO:0004872; F:receptor activity; IEA.  
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.



DR GO: 0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: 0004872; F:receptor activity; IEA.  
 DR GO: 0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003962; FNIII subd.  
 DR InterPro: IPR003961; FNIII  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR003599; IG-  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG c2.  
 DR InterPro: IPR001005; MY5 DNA binding.  
 DR InterPro: IPR003595; PTPC motif.  
 DR InterPro: IPR000387; TYR phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00047; fn3, 7.  
 DR Pfam: PF00047; ig, 3.  
 DR PRINTS: PR00102; Y\_PTPase; 2.  
 DR PRINTS: PR00014; FNTYPEIII.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 6.  
 DR SMART: SM00408; IGc2; 3.  
 DR SMART: SM00194; PTPC; 2.  
 DR SMART: SM00409; IGc2; 3.  
 DR SMART: SM00194; PTPC; 2.  
 DR SMART: SM00404; PTPC\_motif; 2.  
 DR PROSITE: PS00835; IG\_LIKE; 3.  
 DR PROSITE: PS00337; MYB 1; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00386; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Receptor.  
 SQ SEQUENCE 1898 AA; 211673 MW; 034E355624C2FPA7 CRC64;  
  
 Query Match 3.5%; Score 14; DB 4; Length 1898;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 357 VHCAGVGRGTGVFI 370  
 DB 1828 VHCAGVGRGTGVFI 1841  
  
 RESULT 37  
 Q9EQ17 PRELIMINARY; PRT; 1898 AA.  
 ID Q9EQ17  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tyrosine phosphatase LAR.  
 GN PTPRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thymus;  
 RX MEDLINE=21135493; PubMed=11241288;  
 RA Tarsowski G., Jankowski A., Hendriks W.J.A.J., Rolink A.G.,  
 RA Ksiegolow P.;  
 RT "Within the hemopoietic system, LAR phosphatase is a T cell lineage-  
 RT specific adhesion receptor-like protein whose phosphatase activity  
 RT appears dispensable for T cell development, repertoire selection and  
 RT function";  
 RL Eur. J. Immunol. 31:832-840(2001).  
 DR EMBL: AF300943; AK40194.1; -;  
 DR HSSP: F18052; 1YFO.  
 DR MGD; MGI:102695; PTPrf.  
 DR GO: 0001678; F:hydrolyase activity; IEA.  
 DR GO: 0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO: 0006470; F:protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003962; FNIII subd.  
 DR InterPro: IPR003961; FNIII  
 DR InterPro: IPR008957; FN\_III-like.

DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG c2.  
 DR InterPro: IPR000387; TYR phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00047; fn3, 7.  
 DR Pfam: PF00047; ig, 3.  
 DR Pfam: PF00102; Y\_PTPase; 2.  
 DR PRINTS: PR00102; Y\_PTPase; 2.  
 DR PRINTS: PR00014; FNTYPEIII.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 6.  
 DR SMART: SM00408; IGc2; 2.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00835; IG\_LIKE; 3.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00386; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolyase; Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 1898 AA; 211504 MW; EFD48DD11B352A4A CRC64;  
  
 Query Match 3.5%; Score 14; DB 11; Length 1898;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 357 VHCAGVGRGTGVFI 370  
 DB 1828 VHCAGVGRGTGVFI 1841  
  
 RESULT 38  
 Q64604 PRELIMINARY; PRT; 1898 AA.  
 ID Q64604  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protein-tyrosine phosphatase, receptor-type, F polypeptide precursor  
 DE (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related) (Leukocyte  
 DE common antigen-related phosphatase) (Protein-tyrosine-phosphatase)  
 DE (Phosphotyrosine phosphatase) (PTPase).  
 GN LAR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;  
 RX MEDLINE=94347119; PubMed=8068021;  
 RA Zhang W.R., Hashimoto N., Ahmad F., Ding W., Goldstein B.J.;  
 RT "Molecular cloning and expression of a unique receptor-like protein-  
 RT tyrosine-phosphatase in the leukocyte-common-antigen-related phosphatase  
 RT family";  
 RL Biochem. J. 302:39-47(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS PRLAR4.0 AND PRLAR631).  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=HIPPOCAMPUS;  
 RX MEDLINE=95145548; PubMed=7844155;  
 RA Zhang J.S., Longo F.M.;  
 RT "LAR tyrosine phosphatase receptor: alternative splicing is  
 RT preferential to the nervous system, coordinated with cell growth and  
 RT generates novel isoforms containing extensive CAG repeats.";  
 RL J. Cell Biol. 128:415-431(1995).  
 RN [3]  
 RP SEQUENCE OF 1035-1898 FROM N.A., AND MUTAGENESIS.  
 RC TISSUE=HYPOPHALAMUS;  
 RX MEDLINE=92011772; PubMed=1918076;  
 RA Pot D.A., Woodford T.A., Remboutsika E., Haun R.S., Dixon J.E.;  
 RT "Cloning, bacterial expression, purification, and characterization of  
 RT the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine  
 RT phosphatase";  
 RL J. Biol. Chem. 266:19688-19696(1991).  
 CC -!- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR. IT  
 CC POSSSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY



RT protein tyrosine phosphatase in the thymus.";  
 RL J. Immunol. 153:4478-4487(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BAUB/C; TISSUE=EMBRYONIC KIDNEY;  
 RX MEDLINE=95112841; PubMed=7529177;  
 RA Wagner J., Boerboom D., Tremblay M.L.;  
 RT "Molecular cloning and tissue-specific RNA processing of a murine  
 receptor-type protein tyrosine phosphatase.";  
 RL Eur. J. Biochem. 226:773-782(1994).  
 CC -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF T LYMPHOCTE  
 DIFFERENTIATION AND IN EARLY NEURAL DEVELOPMENT. INTERACTS WITH  
 LAR-INTERACTING PROTEIN LIP.1 (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATASE + H(2)O = PROTEIN  
 TYROSINE + ORTHOPHOSPHATE.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=3;  
 Comment=Additional isoforms seem to exist;  
 Name=RPTP-SIGMA T;  
 IsoId=Q64699-1; Sequence=VSP\_050396;  
 Name=RPTP-SIGMA S;  
 IsoId=Q64699-2; Sequence=VSP\_050397;  
 Name=RPTP-SIGMA B;  
 IsoId=Q64699-3; Sequence=VSP\_050395;  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, THYMUS, LUNG, KIDNEY, AND  
 HEART. WEAK EXPRESSION IN SPLEEN. RPTP-SIGMA T IS THE DOMINANT  
 FORM IN THE THYMUS, AND RPTP-SIGMA B IS DOMINANT IN THE BRAIN.  
 CC -!- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-LIKE  
 DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A  
 CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.  
 CC EMBL; D28530; BAA05886.1; -;  
 DR EMBL; D28531; BAA05887.1; -;  
 DR EMBL; X82288; CAA57732.1; -;  
 DR HSSP; P18052; IYFO.  
 DR MGD; MGI:97815; Ptptr.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005194; F:cell adhesion molecule activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004727; F:phosphatase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007155; F:cell adhesion; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_C2.  
 DR InterPro; IPR000387; Tyr\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 8.  
 DR Pfam; PF00047; ig; 3.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00014; FNTPETIII.  
 DR PRINTS; PR00700; PTPHPTASE.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 KW Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 1904 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-  
 TYPE, S.  
 FT DOMAIN 30 1258 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1259 1279 POTENTIAL.  
 FT DOMAIN 1280 1904 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 47 114 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 149 214 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 246 305 IG-LIKE C2-TYPE DOMAIN.

DOMAIN 316 410 FIBRONECTIN TYPE-III.  
 FT DOMAIN 413 509 FIBRONECTIN TYPE-III.  
 FT DOMAIN 512 602 FIBRONECTIN TYPE-III.  
 FT DOMAIN 605 704 FIBRONECTIN TYPE-III.  
 FT DOMAIN 707 809 FIBRONECTIN TYPE-III.  
 FT DOMAIN 812 902 FIBRONECTIN TYPE-III.  
 FT DOMAIN 904 1008 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1011 1125 FIBRONECTIN TYPE-III.  
 FT DOMAIN 628 631 POLY-PRO.  
 FT DOMAIN 893 896 POLY-ALA.  
 FT DOMAIN 960 963 POLY-ALA.  
 FT DOMAIN 1370 1613 PROTEIN-TYROSINE PHOSPHATASE.  
 FT DOMAIN 1656 1904 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT SITE 1545 BY SIMILARITY.  
 FT ACT SITE 1836 BY SIMILARITY.  
 FT DISULFID 54 107 POTENTIAL.  
 FT DISULFID 156 207 POTENTIAL.  
 FT DISULFID 253 298 POTENTIAL.  
 FT VARSPPLIC 623 1010 MISSING (in isoform RPTP-SIGMA B).  
 FT VARSPPLIC 624 630 /FTID=VSP\_050395.  
 FT VARSPPLIC 631 1904 /FTID=VSP\_050396.  
 FT VARSPPLIC 631 1904 Missing (in isoform RPTP-SIGMA S).  
 FT CONFLICT 758 758 P -> A (IN REF. 2).  
 FT CONFLICT 834 834 A -> A (IN REF. 2).  
 FT CONFLICT 853 853 A -> R (IN REF. 2).  
 FT CONFLICT 887 887 A -> G (IN REF. 2).  
 FT CONFLICT 981 981 A -> G (IN REF. 2).  
 FT CONFLICT 1169 1171 RSL -> QHV (IN REF. 2).  
 FT CONFLICT 1518 1518 G -> GVPE (IN REF. 2).  
 FT CONFLICT 1606 1606 G -> S (IN REF. 2).  
 SQ SEQUENCE 1904 AA; 211577 MM; 276B40675B8B37FC CRC64;  
 Query Match 3.5%; Score 14; DB 11; Length 1904;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGVFI 370  
 DB 1834 VHCAGVGRGVFI 1847  
 RESULT 40  
 O44328 PRELIMINARY; PRT; 2051 AA.  
 AC O44328;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 GN HMLAE2.  
 OS Hirudo medicinalis (Medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 CX NCB1\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98195364; PubMed=9526016;  
 RA Gershon T.R., Baker M.W., Nitsbach M., Wu P., Macagno E.R.;  
 RT "Two receptor tyrosine phosphatases of the LAR family are expressed in  
 the developing leech by specific central neurons as well as select  
 peripheral neurons, muscles, and other cells.";  
 RL J. Neurosci. 18:2991-3002(1998).  
 DR EMBL; AF017083; AAB91460.1; -;  
 DR PIR; T30938; T30938.  
 DR HSSP; P28827; IRLPM.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FN\_III.



OC Myxinidae; Eptatretinae; Eptatretus.  
OX NCBI\_TaxID=7764;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20219325; PubMed=10754074;  
RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
RT divergence of tissue-specific isoform genes in the early evolution of  
RT vertebrates.";  
RL J. Mol. Evol. 50:302-311(2000).  
DR EMBL; AB033569; BAA95176.1; -.  
DR HSSP; P18052; 1YFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_PTPase.  
DR Pfam; PF00102; Y\_PTPase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR PRINTS; PR00700; PRTYPHTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
FT NON TER 1  
SQ SEQUENCE 469 AA; 53435 MW; 35BB50A99B992C9 CRC64;  
Query Match 3.2%; Score 13; DB 13; Length 469;  
Best Local Similarity 100.0%; Pred. No. 8.6e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 357 VHCAGVGRGTGV 369  
DB 399 VHCAGVGRGTGV 411  
RESULT 44  
Q9JLJ6 PRELIMINARY; PRT; 112 AA.  
ID Q9JLJ6  
AC Q9JLJ6  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PTP36-D isoform.  
GN PTPN14.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=DDY;  
RA Aoyama K., Matsuda T., Aoki N.;  
RT "Characterization of newly identified four isoforms for a putative  
RT cytosolic protein tyrosine phosphatase PTP36.";  
RL Biochem. Biophys. Res. Commun. 266:523-531(1999).  
DR EMBL; AF170905; AAF27551.1; -.  
DR HSSP; P18052; 1YFO.  
DR MGD; MGI:102467; Ptpn14.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003595; PTPC motif.  
DR InterPro; IPR000387; TYR\_PTPase.  
DR Pfam; PF00102; Y\_PTPase; 1.  
DR PRINTS; PR00700; PRTYPHTASE.  
DR SMART; SM00404; PTPC motif; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.

SQ SEQUENCE 112 AA; 13195 MW; BD4656A8512B3466 CRC64;  
Query Match 3.0%; Score 12; DB 11; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.00028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 357 VHCAGVGRGTGV 368  
DB 44 VHCAGVGRGTGV 55  
RESULT 45  
O02048 PRELIMINARY; PRT; 184 AA.  
ID O02048  
AC O02048  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE T2086.1 protein.  
GN T2086.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Bristol N2;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Bristol N2;  
RA Beck C., Wamsley P.;  
RT "The sequence of C. elegans cosmid T2086.";  
RN [3]  
RP Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RX STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF000193; AAB52889.1; -.  
DR PIR; T15125; T15125.  
DR HSSP; P18052; 1YFO.  
DR WormPep; T2086.1; CE13774.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_PTPase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00102; Y\_PTPase; 1.  
DR PRINTS; PR00700; PRTYPHTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.  
SQ SEQUENCE 184 AA; 20647 MW; 7E478D262B77EA57 CRC64;  
Query Match 3.0%; Score 12; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 356 LVHCSAGVGRTG 367  
 |||||  
 DB 155 LVHCSAGVGRTG 166

## RESULT 46

Q61373 PRELIMINARY; PRT; 361 AA.  
 AC Q61373;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 D2 Protein tyrosine phosphatase (Fragment).  
 GN PTPRJ OR PTP-RL9.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57/BL6; TISSUE=Liver;  
 RA Higashitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,  
 RA Takenawa J., Nakayama H., Fujita J.;  
 RT "Enhanced expression of multiple protein tyrosine phosphatases in the  
 RT regenerating mouse liver: Isolation of PTP-RL 10, a novel  
 RT cytoplasmic-type phosphatase with sequence homology to cytoskeletal  
 RT protein 4.1.";  
 RL Oncogene 0:0-0(1995).  
 DR EMBL; D49393; AAA08386.1; -;  
 DR HSSP; P18052; LYFO.  
 DR MGD; MGI:104574; Ptpn13.  
 DR GO; GO:0007507; P:heart development; IMP.  
 DR GO; GO:0001570; P:vasculogenesis; IMP.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase.

FT NON TER

SQ SEQUENCE 361 AA; 41726 MW; B5146258D11023AA CRC64;

Query Match 3.0%; Score 12; DB 11; Length 361;

Best Local Similarity 100.0%; Pred.No. 0.00081;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRTG 367

|||||

DB 260 LVHCSAGVGRTG 271

## RESULT 47

Q95Y26 PRELIMINARY; PRT; 456 AA.

AC Q95Y26;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 D2 Hypothetical protein.  
 GN Y4104A.5

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
 RX None;

RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
 RA Geisel C., Edwards J., Lamar B.;

RT "The sequence of C. elegans cosmid Y41D4A.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
 RA Waterston R.;

RT "Direct Submission.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC024775; AAK68455.1; -;  
 DR WormPep; Y41D4A.5; CE28359.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000387; Tyr\_phosphatase.

DR InterPro; IPR000242; Tyr\_PP.

DR PRINTS; PR00102; Y\_phosphatase; 1.

DR SMART; SM00194; PTPC; 1.

DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.

DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.

KW Hypothetical protein; Hydrolase.

SQ SEQUENCE 456 AA; 51825 MW; D59783D544296E32 CRC64;

Query Match 3.0%; Score 12; DB 5; Length 456;

Best Local Similarity 100.0%; Pred.No. 0.001;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRTG 367

|||||

DB 290 LVHCSAGVGRTG 301

## RESULT 48

Q9ULJ8 PRELIMINARY; PRT; 849 AA.

AC Q9ULJ8;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 D2 PTP36-B isoform.  
 GN PTPN14.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=DDY;  
 RX MEDLINE=20068798; PubMed=10600535;

RA Aoyama K., Matsuda T., Aoki N.;

RT "Characterization of newly identified four isoforms for a putative

RT cytosolic protein tyrosine phosphatase PTP36.";

RL Biochem. Biophys. Res. Commun. 286:523-531(1999).

DR EMBL; AF170903; AAF27549.1; -;  
 DR HSSP; Q06124; 2SHP.

DR MGD; MGI:102467; Ptpn14.

DR GO; GO:0005856; C:cytoskeleton; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000299; Band 4.1.

DR InterPro; IPR000387; Tyr\_PP.

DR Pfam; PF00373; Band 41; I.

DR Pfam; PF00102; Y\_phosphatase; 1.



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FT DOMAIN 419 486 FIBRONECTIN TYPE-III.
FT DOMAIN 505 575 FIBRONECTIN TYPE-III.
FT DOMAIN 597 672 FIBRONECTIN TYPE-III.
FT DOMAIN 701 787 FIBRONECTIN TYPE-III.
FT DOMAIN 940 1216 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT SITE 1118 1118 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 108 108 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 496 496 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 508 508 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 517 517 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 549 549 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 640 640 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 651 651 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 703 703 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 789 789 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1216 AA; 134275 MW; 406193B108E53591 CRC64;

Query Match 3.0%; Score 12; DB 11; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 LVHCSAGVGRGTG 367
Db 1115 LVHCSAGVGRGTG 1126

RESULT 51
ID O17889 PRELIMINARY; PRT; 1217 AA.
AC O17889;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE F54F12.1 protein.
GN F54F12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";

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RL Science 282:2012-2018 (1998).
DR EMBL; Z81548; CAB04464.1; -.
DR PIR; T22672; T22672.
DR HSSP; P18052; 1YFO.
DR WormRep; F54F12.1; C216114.
DR GO; GO:0016787; F-hydrolase activity; IEA.
DR GO; GO:0004725; P-protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P-protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 1217 AA; 135500 MW; 1D1656F460B38508 CRC64;

Query Match 3.0%; Score 12; DB 5; Length 1217;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 LVHCSAGVGRGTG 367
Db 1068 LVHCSAGVGRGTG 1079

RESULT 52
ID Q8K3Q2 PRELIMINARY; PRT; 1238 AA.
AC Q8K3Q2;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE PTPRJ.
GN PTPRJ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA van Wezel T., Ruivenkamp C.A.L., Zanon C., Staassen A.P.M., Vlcek C.,
RA Caios T., Tripodis N., Groot P.C., Dauwerse H., van Ommen G.J.B.,
RA Demant P.;
RT "Positional cloning identifies Ptprij as the candidate for colon cancer
RT susceptibility QTL Sccl.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039232; AAK98640.1; -.
DR MGD; MGI:104574; Ptprij.
DR GO; GO:0007507; P-heart development; IMP.
DR GO; GO:0001570; P-vasculogenesis; IMP.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 8.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC_motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
SQ SEQUENCE 1238 AA; 136772 MW; 0D02F5BF8E23C0B2 CRC64;

Query Match 3.0%; Score 12; DB 11; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 356 LVHCSAGVGRGTG 367
Db 1137 LVHCSAGVGRGTG 1148

RESULT 53
Q8C1W9 PRELIMINARY; PRT; 1238 AA.
AC Q8C1W9
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Protein tyrosine phosphatase receptor-like protein J.
GN PTPRJ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvSl.
RA MEDLINE=22094388; PubMed=12089527;
RX van Wezel T., Ruivenkamp C.A.L., Zanon C., Stassen A.P.M., Vleek C.,
RA Csikos T., Tripodis N., Groot P.C., Bauwerse H., van Ommen G.J.B.,
RA Demant P.;
RT "Ptpri is a candidate for the mouse colon-cancer susceptibility locus
RT Scci and is frequently deleted in human cancers.";
RL Nat. Genet. 31:295-300(2002).
DR EMBL; AY038877; AAN11409.1;
DR EMBL; AY038861; AAN11409.1; JOINED.
DR MGD; MGI:104574; Ptpri.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTP motif.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PTPVPEPTASE.
DR SMART; SM00060; FN3; 8.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW RECEPTOR.
SQ SEQUENCE 1238 AA; 136712 MW; 136712 MW; DC294E2543995B6C CRC64;

Query Match 3.0%; Score 12; DB 11; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367
Db 1137 LVHCSAGVGRGTG 1148

RESULT 54
Q8CIN2 PRELIMINARY; PRT; 1397 AA.
AC Q8CIN2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Receptor-like protein tyrosine phosphatase gamma B-type isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Kruger R.P., Goodyear R.J., Legan P.K., Marchol M., Raphael Y.,
RA Cotanche D.A., Richardson G.P.;
RT "The supporting-cell antigen; a receptor-like protein tyrosine
RT phosphatase expressed in the sensory epithelia of the inner ear.";
RL J. Neurosci. 19:4815-4827(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Legan P.K.;
RN Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97168988; PubMed=9016795;
RA Shintani T., Maeda N., Nishiwaki T., Noda M.;
RT "Characterization of rat receptor-like protein tyrosine phosphatase
RT gamma isoforms.";
RL Biochem. Biophys. Res. Commun. 230:419-425(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Shintani T., Noda M.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY17704; AAN72430.1;
DR GO; GO:0004089; P:carbonate dehydratase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0008270; P:zinc ion binding; IEA.
DR GO; GO:0005730; P:one-carbon compound metabolism; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR001146; Ruk_Coanhd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PTPVPEPTASE.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
SQ SEQUENCE 1397 AA; 156023 MW; 156023 MW; 1B9E7AB2144D4FB9 CRC64;

Query Match 3.0%; Score 12; DB 11; Length 1397;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367
Db 1017 LVHCSAGVGRGTG 1028

RESULT 55
Q9W6V5 PRELIMINARY; PRT; 1406 AA.
AC Q9W6V5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Supporting-cell antigen precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Kruger R.P., Goodyear R.J., Legan P.K., Marchol M., Raphael Y.,
RA Cotanche D.A., Richardson G.P.;
RT "The supporting-cell antigen; a receptor-like protein tyrosine
RT phosphatase expressed in the sensory epithelia of the inner ear.";
RL J. Neurosci. 19:4815-4827(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Legan P.K.;
RN Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ238216; CAB41385.2; --  
 DR HSPF; P18052; tyro.  
 DR GO; GO:0016787; F:Hydrolase activity; IEA.  
 DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00041; fn3; 9.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 9.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 SQ SEQUENCE 1406 AA; 154213 MW; 2D609885CC0F367B CRC64;  
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 Best Local Similarity 100.0%; Pred. No. 0.0029;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 LVHCSAGVGRTG 367  
 DB 1305 LVHCSAGVGRTG 1316  
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 AC Q8CIN3  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Receptor-like protein tyrosine phosphatase gamma A-type isoform.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97168988; PubMed=9016795;  
 RA Shintani T., Maeda N., Nishiwaki T., Noda M.;  
 RT "Characterization of rat receptor-like protein tyrosine phosphatase  
 gamma isoforms.";  
 RL Biochem. Biophys. Res. Commun. 230:419-425 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=21098932; PubMed=11173927;  
 RA Shintani T., Maeda N., Noda M.;  
 RT "Receptor-like protein tyrosine phosphatase gamma (RPTPgamma), but not  
 PTPbeta/RPTPbeta, inhibits nerve-growth-factor-induced neurite  
 outgrowth in PC12 cells.";  
 RL Dev. Neurosci. 23:55-69 (2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Shintani T., Noda M.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; A177703; AAN72429.1; --  
 DR GO; GO:0004089; F:Carbonate dehydratase activity; IEA.  
 DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
 DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR001148; Euk\_Coanhd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.

DR InterPro; IPR003595; PTPC motif.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR Pfam; PF00194; carb anhydriase; 1.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR PRODOM; PD000865; Euk\_Coanhd; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR SMART; SM00404; PTPC motif; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 SQ SEQUENCE 1426 AA; 159196 MW; 24A5FBBA0F1ED378 CRC64;  
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 Best Local Similarity 100.0%; Pred. No. 0.0029;  
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 QY 356 LVHCSAGVGRTG 367  
 DB 1046 LVHCSAGVGRTG 1057  
 RESULT 57  
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 AC Q8IGV3  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RE06719p (CG10975-PB).  
 GN PTP69D OR CG10975.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuroo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celnikier S.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George B.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abrell J.P., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
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 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Gloddek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jaisali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
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 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.N., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*."  
 RT Science 287:2185-2195(2000).  
 RL [3]  
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 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,  
 RA Ciamp M.E., Drysdale R.A., Emert D., Frisse E., de Grey A.D.N.J.,  
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,  
 RA Russo S., Seare S.M.J., Smith E., Shu S., Smutniak P.,  
 RA Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,  
 RA Lewis S.E.  
 RT "Annotation of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT001531; AAN71286.1; -  
 DR EMBL; AB033540; AAO41254.1; -  
 DR FlyBase; FBGN0014007; Ptp69D.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IDA.  
 DR GO; GO:0007415; P:dephosphorylation of motor neuron; IGI.  
 DR GO; GO:0008045; P:motor axon guidance; IGI.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.  
 DR InterPro; IPR003961; FN\_III-like.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR003595; PTPc motif.  
 DR InterPro; IPR003387; TVR Phosphatase.  
 DR InterPro; IPR00242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 3.  
 DR Pfam; PF00047; ig; 2.  
 DR Pfam; PF00102; Y-phosphatase; 2.  
 DR PRINTS; PR00700; PTPYPTPTASE.  
 DR SMART; SM00060; FN3; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00408; IGc2; 2.  
 DR SMART; SM00134; PTPc; 2.  
 DR SMART; SM00404; PTPc motif; 2.  
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 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 DR PROSITE; PS00056; TYR PHOSPHATASE 2; 2.  
 DR PROSITE; PS00055; TYR PHOSPHATASE\_PTP; 2.  
 SQ SEQUENCE 1461 AA; 167372 MW; 655B21C7402065DD CRC64;

Query Match 3.0%; Score 12; DB 5; Length 1461;  
 Best Local Similarity 100.0%; Pred. NO. 0.003;  
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 356 LVHCSAGVGRGTG 367  
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Db 1093 LVHCSAGVGRGTG 1104  
 RESULT 58  
 Q9VU03  
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 AC Q9VU03  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE CG10975 protein.  
 GN PTP69D OR CG10975.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
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 RN [1]  
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 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
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 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
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 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
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 RA Ferreria S., Frisse E., Galle R.F., Garg N.S., George R.A.,  
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 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of Drosophila melanogaster genome";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradscky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Bernier B., Carlson J.W., Celisner S.E.,  
RA Ciamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,  
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Kearse S.M.J., Smith E., Shu S., Smutnicki F., Whitfield E., S.B.;  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.;  
RT "Annotation of Drosophila melanogaster genome";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMEL; AS003540; AAF49892.2; -  
DR HSP; P18052; IYFO.  
DR FlyBase; F8gn0014007; Ptp69D.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IDA.  
DR GO; GO:0007415; P:dephosphorylation of motor neuron; IGI.  
DR GO; GO:0008045; P:motor axon guidance; IGI.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.  
DR InterPro; IPR003961; FN\_III-like.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003595; PTPc motif.  
DR InterPro; IPR00387; TYR\_phosphatase.  
DR InterPro; IPR00242; TYR\_PP.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; IG; 2.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00408; IGC2; 2.  
DR SMART; SM00194; PTPc; 2.  
DR SMART; SM00404; PTPc motif; 2.  
DR PROSITE; PS0835; IG LIKE; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
KW Immunoglobulin domain  
SQ SEQUENCE 1462 AA; 167459 MW; 61214ADC778D319A CRC64;  
  
Query Match 3.0%; Score 12; DB 5; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 356 LVHCSAGVGRTG 367  
Db 1094 LVHCSAGVGRTG 1105  
  
RESULT 59  
Q9ERK5 PRELIMINARY; PRT; 1705 AA.  
AC Q9ERK5  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)  
DE Osteostesticular protein tyrosine phosphatase (EC 3.1.3.48).  
GN PTPRV OR ESP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone;  
RX MEDLINE=20534790; PubMed=11080586;  
RA Morrison D.F., Mauro L.J.;  
RT "Structural characterization and chromosomal localization of the mouse  
cDNA and gene encoding the bone tyrosine phosphatase, MOST-PTP";  
RL Gene 257:195-208(2000).  
DR EMEL; AE300701; AAG28768.1; -  
DR HSP; P18052; IYFO.  
DR MGD; MGI:108027; Ptpv.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004727; F:phosphorylated protein tyrosine phosphatase act. .; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003961; FN\_III-like.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00041; fn3; 7.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 7.  
DR SMART; SM00194; PTPc; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
SQ SEQUENCE 1705 AA; 186810 MW; 84A8BFA812EE53C1 CRC64;  
  
Query Match 3.0%; Score 12; DB 11; Length 1705;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 356 LVHCSAGVGRTG 367  
Db 1347 LVHCSAGVGRTG 1358  
  
RESULT 60  
Q8N470 PRELIMINARY; PRT; 157 AA.  
AC Q8N470  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
DE Similar to protein-tyrosine-phosphatase homolog DKFZp566K0524.1-  
human.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMEL; BC036539; AAH36539.1; -  
SQ SEQUENCE 157 AA; 17838 MW; 48A71A8D89756F45 CRC64;  
  
Query Match 2.7%; Score 11; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 0.0045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 133 QLAQIRPLFN 143  
Db 126 QLAQIRPLFN 136  
  
RESULT 61  
Q23433 PRELIMINARY; PRT; 198 AA.  
ID Q23433





DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CD45 (Fragment)  
 GN CD45  
 OS Xenopus laevis (African clawed frog)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Turpen J., Kelley C., Mead P., Zon L.;  
 RT "Bi-Potential Primitive-Definitive Hematopoietic Progenitors in the  
 RL Vertebrate Embryo";  
 RL Immunity 6:0-0(1997).  
 DR EMBL; AF024438; AAB81279.1; --  
 DR HSSP; P18052; IYFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; Tyr\_PP.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPc; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON\_TER 1 1  
 FT NON\_TER 306 306  
 SQ SEQUENCE 306 AA; 35508 MW; 1696304FC94CP3F8 CRC64;  
 Query Match 2.7%; Score 11; DB 13; Length 306;  
 Best Local Similarity 100.0%; Pred. No. 0.0084;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGRTG 367  
 DB 103 VHCSAGVGRTG 113  
 RESULT 65  
 Q9UBT5  
 ID Q9UBT5 PRELIMINARY; PRT; 377 AA.  
 AC Q9UBT5  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Protein tyrosine phosphatase receptor-type O truncated PTPROT.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99428326; PubMed-10498613;  
 RA Aguiar R.C., Yakushijin Y., Kharbada S., Tiwari S., Freeman G.J.,  
 RA Shipp M.A.;  
 RT "PTPROT: An alternatively spliced and developmentally regulated B-  
 RL lymphoid phosphatase that promotes GO/G1 arrest.";  
 RL Blood 94:2403-2413(1999).  
 DR EMBL; AF187044; AAF04087.1; --  
 DR EMBL; AF187042; AAF04085.1; --  
 DR HSSP; P28827; IRPM.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 DR InterPro; IPR000387; Tyr\_PP.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.

DR SMART; SM00194; PTPc; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Hydrolase; Receptor.  
 SQ SEQUENCE 377 AA; 43760 MW; 42E10120DBF2D1EF CRC64;  
 Query Match 2.7%; Score 11; DB 4; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 YIATQGLPPT 241  
 DB 168 YIATQGLPPT 178  
 RESULT 66  
 Q8MTNO  
 ID Q8MTNO PRELIMINARY; PRT; 383 AA.  
 AC Q8MTNO  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LAR (Fragment)  
 OS Culicoides sonorensis.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematoidea; Chironomoidea;  
 OC Ceratopogonidae; Ceratopogoninae; Culicoides.  
 OX NCBI\_TaxID=179676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Midgut;  
 RA Campbell C.D.;  
 RT "Identification of differentially expressed midgut transcripts in  
 RT Culicoides sonorensis (Diptera: Ceratopogonidae) following an EHDV  
 RT oral feeding.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AV095263; AAM28342.1; --  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003595; PTPc motif.  
 DR InterPro; IPR000387; Tyr\_PP.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPc; 2.  
 DR SMART; SM00404; PTPc motif; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 FT NON\_TER 1 1  
 FT NON\_TER 383 383  
 SQ SEQUENCE 383 AA; 44171 MW; 648B2DC38BF47E96 CRC64;  
 Query Match 2.7%; Score 11; DB 5; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGRTG 367  
 DB 84 VHCSAGVGRTG 94  
 RESULT 67  
 Q62604  
 ID Q62604 PRELIMINARY; PRT; 398 AA.  
 AC Q62604  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN CPT1.  
 OS Rattus norvegicus (Rat).



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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C X A.CA;
RX MEDLINE=96070847; PubMed=7592997;
RA Pixley F.J., Lee P.S.W., Dominguez M.G., Einstein D.B., Stanley E.R.;
RT "A heteromeric protein-tyrosine phosphatase, PTP phi, is regulated
RL by CSP-1 in macrophages";
RJ J. Biol. Chem. 270:27339-27347(1995).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATASE + H(2)O = PROTEIN
CC TYROSINE + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: ISOFORMS 1 AND 3 ARE TYPE III MEMBRANE
CC PROTEINS. ISOFORM 2 IS CYTOPLASMIC.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q60998-1; Sequence=displayed;
CC Name=2;
CC IsoId=Q60998-2; Sequence=VSP_050393;
CC Name=3;
CC IsoId=Q60998-3; Sequence=VSP_050394;
CC -1- TISSUE SPECIFICITY: EXPRESSED AT MODERATE LEVELS IN BRAIN WITH
CC LOWER LEVELS IN KIDNEY, BONE MARROW AND HEART. VERY LOW LEVELS IN
CC LUNG, SPLEEN AND THYMUS. NO EXPRESSION IN LIVER, INTESTINE,
CC STOMACH, SKELETAL MUSCLE, UTERUS OR TESTIS.
CC -1- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
CC EMBL: U37465; AAC52311.1; -
CC EMBL: U37466; AAC52312.1; -
CC EMBL: U37467; AAC52313.1; -
CC F01: I49372; I49372.
CC HSP: P28827; IRPM.
CC MG: MG11097152; Ptpro.
CC GO: GO:0016021; C: integral to membrane; IEA.
CC GO: GO:0016787; F: hydrolase activity; IEA.
CC GO: GO:0004727; F: prenylated protein tyrosine phosphatase act. . ; IEA.
CC GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
CC InterPro: IPR000387; TYR_PTPase.
CC Pfam: PF00102; Y_phosphatase; 1.
CC InterPro: IPR000242; Tyr_PP.
CC PRINTS: PR00700; PRTYPHPTASE.
CC SMART: SM00194; PTPC; 1.
CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Transmembrane; Alternative splicing.
FT DOMAIN 1 8 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 9 33 POTENTIAL.
FT DOMAIN 34 405 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 383 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 325 325 BY SIMILARITY.
FT VARSPPLIC 1 118 Missing (in isoform 2).
FT VARSPPLIC 66 94 /FTid=VSP_050393.
FT VARSPPLIC 66 94 /FTid=VSP_050394.
FT SEQUENCE 405 AA; 46948 MW; 0DA781001E1E252 CRC64;
Query Match 2.7%; Score 11; DB 11; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 YIATQGLPET 241
DB 196 YIATQGLPET 206
RESULT 71
Q8J1Q4 PRELIMINARY; PRT; 419 AA.
AC Q8J1Q4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein tyrosine phosphatase e (Fragment).
GN PTPe.

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OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphs; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HNI;
RX MEDLINE=22133319; PubMed=12137956;
RA Okubo K., Mitani H., Naruse K., Kondo M., Shima A., Tanaka M.,
RA Asakawa S., Shimizu N., Yoshiura Y., Aida K.;
RT "Structural characterization of GNRH loci in the medaka genome.";
RL Gene 293:181-189(2002).
DR EMBL: AB074501; BAC06424.1; -
DR GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.
DR GO: GO:0005351; F: sugar porter activity; IEA.
DR GO: GO:0009401; P: phenolpyruvate-dependent sugar phospho. . ; IEA.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR InterPro: IPR002114; Hpr_Serp_S.
DR InterPro: IPR003595; PTPC motif.
DR InterPro: IPR000387; TYR_PTPase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 1.
DR SMART: SM00404; PTPC motif; 2.
DR PROSITE: PS00589; PTS_HPR_SER; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 2.
FT NON_TER 1
FT SEQUENCE 419 AA; 46678 MW; 7E6A1F211D305040 CRC64;
Query Match 2.7%; Score 11; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 357 VHCAGVGRTG 367
DB 52 VHCAGVGRTG 62
RESULT 72
Q8MJQ3 PRELIMINARY; PRT; 433 AA.
AC Q8MJQ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD45 phosphatase (Fragment).
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Partial characterization of the CD45 phosphatase cDNA in the owl
RL monkey Aotus vociferans.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF364095; AAM48511.1; -
DR GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003595; PTPC motif.
DR InterPro: IPR000387; TYR_PTPase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 1.

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DR SMART; SM00194; PTPC; 1.  
 DR SMART; SM00404; PTPC motif; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 FT NON\_TER 1  
 FT NON\_TER 433  
 FT NON\_TER 433  
 SQ SEQUENCE 433 AA; 50151 MW; BRAB00C4F008E80D CRC64;

Query Match 2.7%; Score 11; DB 6; Length 433;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASGVGRTG 367  
 DB 387 VHCASGVGRTG 397

RESULT 73  
 Q64642 PRELIMINARY; PRT; 438 AA.  
 AC Q64642;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Brain-enriched membrane-associated protein tyrosine phosphatase 2  
 DE (EC 3.1.3.48) (BWM-2) (Protein-tyrosine-phosphatase) (Phosphotyrosine phosphatase) (PTPase) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-BRAIN;  
 RA Itoh S.; Okada M.; Nakagawa H.;  
 RT Isolation and characterization of a novel membrane-associated protein tyrosine phosphatase-like protein expressed preferentially in the central nervous system."  
 RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + PHOSPHATE.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE TYPE III RPTP FAMILY.  
 DR EMBL; D45413; BAA08253.1; -.  
 DR HSSP; P18052; 1VFO.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004727; F:phosphorylated protein tyrosine phosphatase act. .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR00387; TYR\_phosphatase.  
 DR InterPro; IPR00242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; FALSE NEG.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Glycoprotein; Transmembrane; Repeat; Hydrolase; Receptor.  
 FT NON\_TER 1  
 FT DOMAIN <1 72 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN <1 49 FIBRONECTIN TYPE-III.  
 FT TRANSMEM 73 93 POTENTIAL.  
 FT DOMAIN 94 438 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 157 395 PROTEIN-TYROSINE PHOSPHATASE.  
 FT ACT\_SITE 328 338 BY SIMILARITY.  
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 438 AA; 49205 MW; 55B7025A479D6A7 CRC64;

Query Match 2.7%; Score 11; DB 11; Length 438;

Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASGVGRTG 367  
 DB 336 VHCASGVGRTG 346

RESULT 74  
 Q9NL06 PRELIMINARY; PRT; 468 AA.  
 AC Q9NL06;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE HGTPR2AB protein (Fragment).  
 GN HGTPR2AB.  
 OS Eptatretus burgeri (Inshore hagfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes; Myxinidae; Eptatretinae; Eptatretus.  
 NCBI\_TaxID=7764;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20219325; PubMed=10754074;  
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray: divergence of tissue-specific isoform genes in the early evolution of vertebrates."  
 RT J. Mol. Evol. 50:302-311(2000).  
 DR EMBL; AB033571; BAA95178.1; -.  
 DR HSSP; P18052; 1VFO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR00387; TYR\_phosphatase.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase.  
 FT NON\_TER 1  
 SQ SEQUENCE 468 AA; 53952 MW; 7F123B7D3EAD69D CRC64;

Query Match 2.7%; Score 11; DB 13; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASGVGRTG 367  
 DB 107 VHCASGVGRTG 117

RESULT 75  
 Q9NL14 PRELIMINARY; PRT; 469 AA.  
 AC Q9NL14;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE AMPTPR4B protein (Fragment).  
 GN AMPTPR4B.  
 OS Branchiostoma belcheri (Amphioxus).  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.  
 NCBI\_TaxID=7741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20219325; PubMed=10754074;  
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:

RT divergence of tissue-specific isoform genes in the early evolution of

RT vertebrates.";  
RL J. Mol. Evol. 50:302-311 (2000).  
DR EMEL; AB033563; BAA95170.1; -.  
DR HSSP; P18052; IYFO.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR001664; IF.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_Pp.  
DR Pfam; PF00102; y\_phosphatase; 2.  
DR PRINTS; PR00700; PRTPHPTASE.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00226; IF; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
FT NON TER  
SQ SEQUENCE 469 AA; 53631 MW; C2CBED629815317 CRC64;

Query Match 2.78; Score 11; DB 5; Length 469;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCSAGVGRGTG 367  
|||  
Db 106 VHCSAGVGRGTG 116

Search completed: June 21, 2004, 17:26:29  
Job time : 49 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 17:13:38 ; Search time 58 Seconds  
(without alignments)  
1972.961 Million cell updates/sec

Title: US-09-095-478a-7

Perfect score: 405

Sequence: 1 MESPRLKVGKGRDNDEEG.....DIMNVITQMRQRGMQTK 405

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A\_Geneseqp\_29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	405	2	AaW89251 Mouse PTP
2	405	100.0	426	2	AaW89249 Mouse PTP
3	362	89.4	463	2	AaW89250 Mouse PTP
4	29	7.2	29	2	AaW89264 Human PTP
5	29	7.2	29	2	AaW89263 Human PTP
6	29	7.2	29	2	AaW89265 Human PTP
7	23	5.7	122	2	AaW89252 Rat PTP10
8	19	4.7	261	6	Aae37994 Human Kin
9	19	4.7	398	5	Abg30845 Human tyr
10	19	4.7	398	7	Add89795 Human DKF
11	19	4.7	409	7	Adg09123 Novel pro
12	19	4.7	412	6	Aae37996 Human kin
13	19	4.7	420	5	Aae14454 Human pro
14	19	4.7	508	7	Adg08106 Novel pro
15	19	4.7	561	4	Abg06042 Novel hum
16	15	3.7	272	2	AaW67441 N-terminu
17	15	3.7	272	2	Aay34161 Human PTP
18	15	3.7	1105	4	Aam25567 Human pro
19	15	3.7	1174	2	AaW67438 Human pro
20	15	3.7	1174	2	Aay34158 Human pro
21	15	3.7	1174	7	Add45494 Human Pro
22	15	3.7	1175	7	Adg83529 Rat Prote
23	15	3.7	1175	7	Adg61029 Rat Prote
24	15	3.7	1175	7	Adg61033 Rat Prote
25	14	3.5	176	2	AaW60876 Product o

26	14	3.5	245	4	AAB59389	Human pro
27	14	3.5	294	4	AAG78287	Human BCA
28	14	3.5	322	4	AAR60877	Product o
29	14	3.5	442	3	AAB56372	Human pro
30	14	3.5	607	3	AAY81783	Human pro
31	14	3.5	607	3	AAY56098	LAR tyros
32	14	3.5	647	4	AAM23746	Human EST
33	14	3.5	647	4	AAU14379	Human nov
34	14	3.5	1291	5	AAR75201	Tyrosine
35	14	3.5	1495	5	ABB57380	Rat mucoc
36	14	3.5	1496	7	ADE57115	Rat Prote
37	14	3.5	1496	7	ADE57119	Rat Prote
38	14	3.5	1496	7	ADD47013	Rat Prote
39	14	3.5	1501	7	ADD47017	Rat Prote
40	14	3.5	1796	6	AEE37971	Human kin
41	14	3.5	1863	7	ADD46989	Rat Prote
42	14	3.5	1897	3	AAY81785	Human pro
43	14	3.5	1897	3	AAY56100	LAR tyros
44	14	3.5	1897	3	AAB19712	Human pro
45	14	3.5	1897	3	ADD18740	Human dis
46	14	3.5	1897	3	ABE57100	Mouse lac
47	14	3.5	1904	5	ABE57100	Mouse lac
48	14	3.5	1907	4	AAU14143	Human nov
49	14	3.5	1911	2	AAR71726	Human PTP
50	14	3.5	1911	2	AAW27225	Human pro
51	14	3.5	1911	2	AAW94027	Human pro
52	14	3.5	1911	2	AU01459	Human pro
53	14	3.5	1948	7	ADD18742	Human dis
54	14	3.5	1949	7	ADE57117	Human pro
55	14	3.5	1949	7	ADE57121	Human pro
56	14	3.5	1949	7	ADD47019	Human pro
57	14	3.5	1949	7	ADD47015	Human pro
58	14	3.5	1959	6	Aae37322	Human rec
59	14	3.5	2281	5	AAO18736	Human NOV
60	14	3.5	2291	5	ABP60057	Human pro
61	14	3.5	2299	6	AG79724	Human KRP
62	14	3.5	2299	6	AG79724	Human KRP
63	14	3.5	2300	5	AAO18738	Human NOV
64	14	3.5	2301	6	ABP60058	Human pro
65	12	3.0	14	4	ABE56552	Human SNP
66	12	3.0	245	2	AAR20747	Human R-P
67	12	3.0	257	4	AAB59381	Drosophil
68	12	3.0	263	4	AG78279	Drosophil
69	12	3.0	263	4	AAB59368	Human PTP
70	12	3.0	319	4	AG78266	Human PTP
71	12	3.0	1337	2	AAR85203	huDBP-1.
72	12	3.0	1428	4	ABE65364	Drosophil
73	12	3.0	1445	2	AAR58809	Human RPT
74	12	3.0	1705	5	ABE52348	Protein r
75	12	3.0	1711	2	AAW70506	Osteotest
76	12	3.0	1711	5	ABE52349	Protein r
77	11	2.7	11	2	AAY34167	PTP-Di bi
78	11	2.7	12	3	AAY81786	Protein t
79	11	2.7	197	3	AAB37997	Human kin
80	11	2.7	226	6	AAB37993	Human kin
81	11	2.7	236	2	AAO4700	Human RPT
82	11	2.7	236	2	AAO4700	Mouse RPT
83	11	2.7	240	7	ADD22988	Human pro
84	11	2.7	248	7	ADD22988	Human pro
85	11	2.7	250	4	AAB59370	Human pro
86	11	2.7	250	4	AAB59387	Yeast pro
87	11	2.7	253	4	AAB59374	Murine pr
88	11	2.7	253	4	AAB59373	Human pro
89	11	2.7	254	4	AAB59377	Human pro
90	11	2.7	254	4	AAB59386	Yeast pro
91	11	2.7	254	4	AAB59372	Human pro
92	11	2.7	255	4	AAB59379	Human pro
93	11	2.7	257	4	AAB59369	Drosophil
94	11	2.7	260	4	AAB59388	Human pro
95	11	2.7	261	4	AAB59367	Human pro
96	11	2.7	261	4	AAB59366	Human pro
97	11	2.7	274	7	AAB59385	Protein t
98	11	2.7	296	7	ABW78984	Human leu

99 11 2.7 306 4 AAG78268 Human DCA  
100 11 2.7 307 4 AAG78285 Fission y

## ALIGNMENTS

RESULT 1  
AAW89251  
ID AAW89251 standard; protein; 405 AA.  
AC AAW89251;  
XX

DT 10-MAR-1999 (first entry)  
XX

DE Mouse PTP05 isoform #2.  
XX

KW PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease.  
XX

OS Mus sp.  
XX

PN WO9849317-A2.  
XX

PD 05-NOV-1998.  
XX

PF 27-APR-1998; 98WO-US008439.  
XX

PR 28-APR-1997; 97US-0044428P.  
XX

PR 20-MAY-1997; 97US-0047222P.  
XX

PR 11-JUN-1997; 97US-0049477P.  
XX

PR 11-JUN-1997; 97US-0049756P.  
XX

PR 18-JUN-1997; 97US-0049914P.  
XX

PR 23-OCT-1997; 97US-0063595P.  
XX

PA (SUGEN) SUGEN INC.  
XX

PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
XX

PI Courtneidge SA, App H, Hui TH;  
XX

XX WPI; 1999-009434/01.  
XX

DR N-PSDB; AAV81746.  
XX

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful  
PT for identifying specific modulators for treatment and prevention of  
PT cancer and neurodegenerative disease.  
XX

PS Claim 2; Page 158-160; 193pp; English.  
XX

CC The present invention describes isolated, enriched or purified nucleic  
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
CC present sequence represents mouse PTP05. The above proteins, other than  
CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
CC substances that modulate their activity (i.e. agonists and antagonists,  
CC including NBP) in vivo or in vitro. These substances are used to treat or  
CC prevent diseases associated with abnormal signal transduction pathways  
CC that involve the proteins, particularly cancer (e.g. leukaemia and  
CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
CC serine/threonine kinase) are used to promote neuronal survival,  
CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
CC proteins can be used as probes to identify and clone related sequences;  
CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
CC therapy (optionally after mutation). Ab are used to determine the  
CC proteins  
XX

SQ Sequence 405 AA;  
XX

Query Match 100.0%; Score 405; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRDNDDEEGNSGNLIRNSI.PSSSOKMTTKDIFGNKMSENVKPSHLL 60  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 60  
1 MSSPRKVRGKTGRDNDDEEGNSGNLIRNSI.PSSSOKMTTKDIFGNKMSENVKPSHLL 60  
QY 61 SPSDKYELVYPEPLESDTDETVMDVSDRSRLNRWNSMDSETAGPSKTVSPVLSGSRLSK 120  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 120  
61 SPSDKYELVYPEPLESDTDETVMDVSDRSRLNRWNSMDSETAGPSKTVSPVLSGSRLSK 120  
QY 121 DTETSVSEKELTQLAQIRPLIFNSSARSAMDGCLNTLOKKEELDIIRFLELSQMTLPDD 180  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 180  
121 DTETSVSEKELTQLAQIRPLIFNSSARSAMDGCLNTLOKKEELDIIRFLELSQMTLPDD 180  
QY 181 FNSGNTLQNRDKKRYRDILPYDSTRVPLGKNKYINASYIRIVNHEEEXFYIATQGPLPE 240  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 240  
181 FNSGNTLQNRDKKRYRDILPYDSTRVPLGKNKYINASYIRIVNHEEEXFYIATQGPLPE 240  
QY 241 TIEDFWQVLENNCNVMIATRIECCGVKICYWNPISLKEPLEFEPHSPVLETFHTVQY 300  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 300  
241 TIEDFWQVLENNCNVMIATRIECCGVKICYWNPISLKEPLEFEPHSPVLETFHTVQY 300  
QY 301 FTVRVFOIVKKSCTGKSCQVKHLQFTKWPDHGTSPASADFFIKYVYVRKSHITGPLLWHCS 360  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 360  
301 FTVRVFOIVKKSCTGKSCQVKHLQFTKWPDHGTSPASADFFIKYVYVRKSHITGPLLWHCS 360  
QY 361 AGVGTGTFICVDVWVPSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 405  
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 405  
361 AGVGTGTFICVDVWVPSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 405

## RESULT 2

AAW89249  
ID AAW89249 standard; protein; 426 AA.  
XX

AC AAW89249;  
XX

DT 10-MAR-1999 (first entry)  
XX

DE Mouse PTP05.  
XX

KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease.  
XX

OS Mus sp.  
XX

PN WO9849317-A2.  
XX

PD 05-NOV-1998.  
XX

PF 27-APR-1998; 98WO-US008439.  
XX

PR 28-APR-1997; 97US-0044428P.  
XX

PR 20-MAY-1997; 97US-0047222P.  
XX

PR 11-JUN-1997; 97US-0049477P.  
XX

PR 11-JUN-1997; 97US-0049756P.  
XX

PR 18-JUN-1997; 97US-0049914P.  
XX

PR 23-OCT-1997; 97US-0063595P.  
XX

PA (SUGEN) SUGEN INC.  
XX

PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
XX

PI Courtneidge SA, App H, Hui TH;  
XX

XX WPI; 1999-009434/01.  
XX

DR N-PSDB; AAV81744.  
XX

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful  
PT for identifying specific modulators for treatment and prevention of  
PT cancer and neurodegenerative disease.  
XX

PS Claim 2; Page 155-157; 193pp; English.

XX CC The present invention describes isolated, enriched or purified nucleic  
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 CC present sequence represents mouse PTP05. The above proteins, other than  
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
 CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival.  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences,  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins  
 XX SQ Sequence 426 AA;

Query Match 100.0%; Score 405; DB 2; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRSLPSSQKQMTPTKPIFGNKNMSENVPKSHL 60  
 Db 1 MSSPRKVRGKTGRDNDDEEGNSGNLNRSLPSSQKQMTPTKPIFGNKNMSENVPKSHL 60

Qy 61 SFSKDYELVYPEPLESDTDTETVWDVSDRLNRNMSDSETAGPSKTVSPVLGSSRLSK 120  
 Db 61 SFSKDYELVYPEPLESDTDTETVWDVSDRLNRNMSDSETAGPSKTVSPVLGSSRLSK 120

Qy 121 DTTSVSEKLTQAIQIRPLIFNSSARSAMRDLNTLQKKELDIIRFLEQMTLPDD 180  
 Db 121 DTTSVSEKLTQAIQIRPLIFNSSARSAMRDLNTLQKKELDIIRFLEQMTLPDD 180

Qy 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKYINASYIRIVNHEEYFYIATQGLPE 240  
 Db 181 FNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKYINASYIRIVNHEEYFYIATQGLPE 240

Qy 241 TIEDFWQVLENNCNVIAMITREIECGVICKSYWPIISLKEPLEFHFVPLETFHVTQY 300  
 Db 241 TIEDFWQVLENNCNVIAMITREIECGVICKSYWPIISLKEPLEFHFVPLETFHVTQY 300

Qy 301 FTVRVFQIVKSTGKSCVKKHLOFTKWPDHGTPTASADPFKIVRVYRKSHITGPIIVHCS 360  
 Db 301 FTVRVFQIVKSTGKSCVKKHLOFTKWPDHGTPTASADPFKIVRVYRKSHITGPIIVHCS 360

Qy 361 AGVGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCQMIQTK 405  
 Db 361 AGVGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCQMIQTK 405

RESULT 3  
 AAW89250  
 ID AAW89250 standard; protein; 463 AA.  
 XX AC AAW89250;  
 XX DT 10-MAR-1999 (first entry)  
 XX DE Mouse PTP05 isoform #1.  
 XX KW PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
 KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
 KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease.  
 XX OS Mus sp.  
 XX PN W09849317-A2.  
 XX XX  
 XX 05-NOV-1998.

XX PF 27-APR-1998; 98WO-US008439.  
 XX PR 28-APR-1997; 97US-0044428P.  
 PR 20-MAY-1997; 97US-0047222P.  
 PR 11-JUN-1997; 97US-0049477P.  
 PR 11-JUN-1997; 97US-0049756P.  
 PR 18-JUN-1997; 97US-0049914P.  
 PR 23-OCT-1997; 97US-0063595P.  
 XX (SUGGE-) SUGEN INC.  
 XX PA Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
 PI Courtneidge SA, App H, Hui TH;  
 XX WI; 1999-009434/01.  
 DR N-PSDB; AAV81745.  
 XX PT New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 PT for identifying specific modulators for treatment and prevention of  
 PT cancer and neurodegenerative disease.  
 XX PS Claim 2; Page 157-158; 193pp; English.  
 XX CC The present invention describes isolated, enriched or purified nucleic  
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 CC present sequence represents mouse PTP05. The above proteins, other than  
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
 CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival.  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences;  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins  
 XX SQ Sequence 463 AA;

Query Match 89.4%; Score 362; DB 2; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 IFGNKNMSENVPKSHLSFGDKYELVYPEPLESDTDTETVWDVSDRLNRNMSDSETAG 103  
 Db 81 IFGNKNMSENVPKSHLSFGDKYELVYPEPLESDTDTETVWDVSDRLNRNMSDSETAG 140

Qy 104 PSKTVSPVLGSSRLSKDTTSVSEKLTQAIQIRPLIFNSSARSAMRDLNTLQKKEEL 163  
 Db 141 PSKTVSPVLGSSRLSKDTTSVSEKLTQAIQIRPLIFNSSARSAMRDLNTLQKKEEL 200

Qy 164 DIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKYINASYIRIV 223  
 Db 201 DIREFLELEQMTLPDDFNSGNTLQNRDKNRYRDLIPYDSTRVPLGKNKYINASYIRIV 260

Qy 224 NHEEYFYIATQGLPETIEDFWQVLENNCNVIAMITREIECGVICKSYWPIISLKEPL 283  
 Db 261 NHEEYFYIATQGLPETIEDFWQVLENNCNVIAMITREIECGVICKSYWPIISLKEPL 320

Qy 284 EPEHFSVPLETFHVTQYFTRVRFQIVKSTGKSCVKKHLOFTKWPDHGTPTASADPFKIVY 343  
 Db 321 EPEHFSVPLETFHVTQYFTRVRFQIVKSTGKSCVKKHLOFTKWPDHGTPTASADPFKIVY 380

Qy 344 RYVRKSHITGPIIVHCSAGVGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCQMIQ 403  
 Db 381 RYVRKSHITGPIIVHCSAGVGTGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCQMIQ 440

Qy 404 TK 405  
 ||



Db 441 TK 442

RESULT 4  
AAW89264  
ID AAW89264 standard; peptide; 29 AA.

XX AAW89264;  
XX 10-MAR-1999 (first entry)  
XX Human PTP05 peptide 431A.  
XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease.

XX Homo sapiens.

OS WO9849317-A2.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

XX 20-MAY-1997; 97US-0047222P.

XX 11-JUN-1997; 97US-0049477P.

XX 11-JUN-1997; 97US-0049756P.

XX 18-JUN-1997; 97US-0049914P.

XX 23-OCT-1997; 97US-0063595P.

XX (SUGEN-) SUGEN INC.

PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

PI Courtneidge SA, App H, Hui TH;

PI WPI; 1999-009434/01.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful

PT for identifying specific modulators for treatment and prevention of

PT cancer and neurodegenerative disease.

XX Example 14; Page 108; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic

CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

CC above proteins, other than ALK-7, are protein tyrosine phosphatases

CC (PTPs) and are used to identify substances that modulate their activity

CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These

CC substances are used to treat or prevent diseases associated with abnormal

CC signal transduction pathways that involve the proteins, particularly

CC cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is

CC a type I receptor serine/threonine kinase) are used to promote neuronal

CC survival, particularly for treating Alzheimer's, Parkinson's or

CC Huntington's diseases. Nucleic acid fragments of the polynucleotides

CC encoding the proteins can be used as probes to identify and clone related

CC sequences; to detect protein-encoded RNA; to generate transgenic animals

CC and in gene therapy (optionally after mutation). Ab are used to determine

CC the proteins. The present sequence represents a human PTP05 peptide from

XX the present invention

XX Sequence 29 AA;

Query Match 7.2%; Score 29; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.8e-21;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 SPVLGGSSRLSKDTTSVSEKLTQLAQI 137

DB 1 SPVLGGSSRLSKDTTSVSEKLTQLAQI 29

RESULT 5

AAW89263

ID AAW89263 standard; peptide; 29 AA.

XX AAW89263;

XX 10-MAR-1999 (first entry)

XX Human PTP05 peptide 433A.

XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

KW neurodegenerative disease; neuronal survival; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease.

XX Homo sapiens.

OS WO9849317-A2.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-US008439.

XX 28-APR-1997; 97US-0044428P.

XX 20-MAY-1997; 97US-0047222P.

XX 11-JUN-1997; 97US-0049477P.

XX 11-JUN-1997; 97US-0049756P.

XX 18-JUN-1997; 97US-0049914P.

XX 23-OCT-1997; 97US-0063595P.

XX (SUGEN-) SUGEN INC.

PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;

PI Courtneidge SA, App H, Hui TH;

PI WPI; 1999-009434/01.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful

PT for identifying specific modulators for treatment and prevention of

PT cancer and neurodegenerative disease.

XX Example 14; Page 108; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic

CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The

CC above proteins, other than ALK-7, are protein tyrosine phosphatases

CC (PTPs) and are used to identify substances that modulate their activity

CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These

CC substances are used to treat or prevent diseases associated with abnormal

CC signal transduction pathways that involve the proteins, particularly

CC cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is

CC a type I receptor serine/threonine kinase) are used to promote neuronal

CC survival, particularly for treating Alzheimer's, Parkinson's or

CC Huntington's diseases. Nucleic acid fragments of the polynucleotides

CC encoding the proteins can be used as probes to identify and clone related

CC sequences; to detect protein-encoded RNA; to generate transgenic animals

CC and in gene therapy (optionally after mutation). Ab are used to determine

CC the proteins. The present sequence represents a human PTP05 peptide from

XX the present invention

XX Sequence 29 AA;

Query Match 7.2%; Score 29; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.8e-21;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSPRKVRGKTGRNDDEEGNSGNLRLN 29

DB 1 MSSPRKVRGKTGRNDDEEGNSGNLRLN 29

RESULT 6

AAW89265  
ID AAW89265 standard; peptide; 29 AA.

XX AC AAW89265;  
XX DT 10-MAR-1999 (first entry)  
XX DE Human PTP05 peptide 432A.  
XX KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease.

XX OS Homo sapiens.

XX PN WO9849317-A2.

XX PD 05-NOV-1998.

XX PF 27-APR-1998; 98WO-US008439.

XX PR 28-APR-1997; 97US-0044428P.

XX PR 20-MAY-1997; 97US-0047222P.

XX PR 11-JUN-1997; 97US-0049477P.

XX PR 11-JUN-1997; 97US-0049756P.

XX PR 18-JUN-1997; 97US-0049914P.

XX PR 23-OCT-1997; 97US-0063595P.

XX PA (SUGB-) SUGEN INC.

XX PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
PI Courtneidge SA, App H, Hui TH;

XX DR WPI: 1999-009434/01.

XX PT New nucleic acid encoding specific protein tyrosine phosphatases - useful  
PT for identifying specific modulators for treatment and prevention of  
PT cancer and neurodegenerative disease.

XX PS Example 14; Page 108; 193pp; English.

XX CC The present invention describes isolated, enriched or purified nucleic  
XX acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
XX above proteins, other than ALK-7, are protein tyrosine phosphatases  
XX (PTPs) and are used to identify substances that modulate their activity  
XX (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These  
XX substances are used to treat or prevent diseases associated with abnormal  
XX signal transduction pathways that involve the proteins, particularly  
XX cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is  
XX a type I receptor serine/threonine kinase) are used to promote neuronal  
XX survival, particularly for treating Alzheimer's, Parkinson's or  
XX Huntington's diseases. Nucleic acid fragments of the polynucleotides  
XX encoding the proteins can be used as probes to identify and clone related  
XX sequences; to detect protein-encoded RNA; to generate transgenic animals  
XX and in gene therapy (optionally after mutation). Ab are used to determine  
XX the proteins. The present sequence represents a human PTP05 peptide from  
XX the present invention

XX SQ Sequence 29 AA;

Query Match 7.2%; Score 29; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.8e-21; Mismatches 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 MDVSDRLNRLNWSMDSETAGSKTVSPV 111  
DB 1 MDVSDRLNRLNWSMDSETAGSKTVSPV 29

RESULT 7

AAW89252

ID AAW89252 standard; protein; 122 AA.

XX AC AAW89252;

XX DT 10-MAR-1999 (first entry)

XX DE Rat PTP10.

XX KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;

KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;

KW neurodegenerative disease; neuronal survival; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease.

XX OS Rattus sp.

XX PN WO9849317-A2.

XX PD 05-NOV-1998.

XX PF 27-APR-1998; 98WO-US008439.

XX PR 28-APR-1997; 97US-0044428P.

XX PR 20-MAY-1997; 97US-0047222P.

XX PR 11-JUN-1997; 97US-0049477P.

XX PR 11-JUN-1997; 97US-0049756P.

XX PR 18-JUN-1997; 97US-0049914P.

XX PR 23-OCT-1997; 97US-0063595P.

XX PA (SUGB-) SUGEN INC.

XX PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
PI Courtneidge SA, App H, Hui TH;

XX DR WPI: 1999-009434/01.

XX DR N-PSDB; AN81747.

XX PT New nucleic acid encoding specific protein tyrosine phosphatases - useful  
PT for identifying specific modulators for treatment and prevention of  
PT cancer and neurodegenerative disease.

XX PS Claim 2; Page 160; 193pp; English.

XX CC The present invention describes isolated, enriched or purified nucleic  
XX acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
XX present sequence represents rat PTP10. The above proteins, other than ALK  
XX -7, are protein tyrosine phosphatases (PTPs) and are used to identify  
XX substances that modulate their activity (i.e. agonists and antagonists,  
XX including NBP) in vivo or in vitro. These substances are used to treat or  
XX prevent diseases associated with abnormal signal transduction pathways  
XX that involve the proteins, particularly cancer (e.g. leukaemia and  
XX lymphoma), while modulators of ALK-7 (which is a type I receptor  
XX serine/threonine kinase) are used to promote neuronal survival,  
XX particularly for treating Alzheimer's, Parkinson's or Huntington's  
XX diseases. Nucleic acid fragments of the polynucleotides encoding the  
XX proteins can be used as probes to identify and clone related sequences;  
XX to detect protein-encoded RNA; to generate transgenic animals and in gene  
XX therapy (optionally after mutation). Ab are used to determine the  
XX proteins

XX SQ Sequence 122 AA;

Query Match 5.7%; Score 23; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 8.7e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 DFFIKYVRYRKSHITGELLVHC 359  
DB 94 DFFIKYVRYRKSHITGELLVHC 116

RESULT 8

AAE37994

ID AAE37994 standard; protein; 261 AA.

XX

AAE37994;  
 06-NOV-2003 (first entry)  
 Human kinase and phosphatase (KPP-39) protein.  
 Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; neurologic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.  
 OS Homo sapiens.  
 XX KW  
 XX KW  
 PN WO2003050084-A2.  
 XX 19-JUN-2003.  
 XX  
 XX 06-DEC-2002; 2002WO-US039126.  
 XX 07-DEC-2001; 2001US-0340233P.  
 PR 19-DEC-2001; 2001US-0343007P.  
 PR 21-DEC-2001; 2001US-0343546P.  
 PR 04-FEB-2002; 2002US-0354388P.  
 PR 15-FEB-2002; 2002US-0357675P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;  
 PI Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;  
 PI Baughn MR, Chawla NK, Lehr-Watson PM, Khare R, Lee S, Hawkins PR;  
 PI Becha SD, Lee SY, Sprague WW, Zebarjadian Y;  
 XX WPI: 2003-532894/50.  
 DR N-PSDB; AAD57366.  
 XX  
 XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX  
 XX Claim 1; Page 242; 282pp; English.  
 XX  
 XX The invention relates to an isolated polypeptide, which is a human kinase  
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for  
 CC diagnosing, treating or preventing disorders associated with aberrant  
 CC expression of KPP, particularly cell proliferative disorders (e.g.  
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal  
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary  
 CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular  
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/  
 CC inflammatory disorders (e.g. AIDS, acquired immune deficiency syndrome,  
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,  
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's  
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,  
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP  
 CC is useful in assessing the effects of exogenous compounds on the  
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is  
 CC useful in gene therapy and for creating transgenic animals to model human  
 CC disease. The present sequence is human KPP protein  
 XX  
 XX Sequence 261 AA;  
 Query Match 4.7%; Score 19; DB 6; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 3e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 192 KNRYEDILPYDSTRVPLGK 210

Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 192 KNRYEDILPYDSTRVPLGK 210

QY 192 KNRYEDILPYDSTRVPLGK 210  
 DB 27 KNRYEDILPYDSTRVPLGK 45

RESULT 9  
 ABG30845  
 ID ABG30845 standard; protein; 398 AA.  
 XX ABG30845;  
 AC ABG30845;  
 XX 21-OCT-2002 (first entry)  
 DT  
 XX Human tyrosine phosphatase protein #1.  
 DE  
 XX Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;  
 KW central nervous system disorder; CNS; cardiovascular disorder; stroke;  
 KW chronic obstructive pulmonary disease; cancer; multiple sclerosis;  
 KW Alzheimer's disease; Huntington's disease; congestive heart failure;  
 KW myocardial infarction; chromosome 10.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200242435-A2.  
 PN  
 XX 30-MAY-2002.  
 PD  
 XX 27-NOV-2001; 2001WO-EP013794.  
 PP  
 XX 27-NOV-2000; 2000US-0252912P.  
 PR  
 XX (FARB ) BAYER AG.  
 PA  
 XX Zhu Z;  
 PI  
 XX WPI: 2002-575236/51.  
 DR N-PSDB; ABX89178.  
 DR  
 XX  
 XX New human tyrosine phosphatase polypeptide, the regulation of which is  
 PT useful for treating obesity, diabetes, cardiovascular or central nervous  
 PT system disorder, chronic obstructive pulmonary disease and cancer.  
 PT  
 XX Claim 25; Fig 2; 145pp; English.  
 PS  
 XX The present invention relates to a new human tyrosine phosphatase  
 CC polypeptide. The invention is useful for the preparation of a medicament  
 CC for modulating the activity of human tyrosine phosphatase in a disease  
 CC such as obesity, diabetes, a central nervous system (CNS) disorder,  
 CC chronic obstructive pulmonary disease, cardiovascular disorder or cancer.  
 CC The invention is useful for treating a human tyrosine phosphatase  
 CC dysfunction related disease, preferably the above mentioned diseases. The  
 CC invention is useful for treating the above mentioned disorders, where the  
 CC CNS disorder is selected from Parkinson's disease, multiple sclerosis,  
 CC stroke, Alzheimer's disease, and Huntington's disease, and the  
 CC cardiovascular disorder is selected from congestive heart failure and  
 CC myocardial infarction. The molecules of the invention are useful in  
 CC diagnostic assays for detecting diseases and abnormalities or  
 CC susceptibility to disease and abnormalities related to the presence of  
 CC mutations in the polynucleotide coding the polypeptide of the invention.  
 CC The present amino acid sequence represents the human tyrosine phosphatase  
 CC protein #1 of the invention. This sequence is encoded by the human  
 CC tyrosine phosphatase gene located on chromosome 10  
 XX  
 XX Sequence 398 AA;  
 Query Match 4.7%; Score 19; DB 5; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 3e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 192 KNRYEDILPYDSTRVPLGK 210

Db 164 KNYRDILPYDSTRVPLGK 182

RESULT 10

ADD89795

ID ADD89795 standard; protein; 398 AA.

XX AC ADD89795;

XX 29-JAN-2004 (first entry)

DE Human DKFP566K0524 protein SEQ ID NO:10.

XX cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;

XX immunosuppressive; antidiabetic; neuroprotective; antirheumatic;

XX antiarthritic; antipsoriatic; antiarteriosclerotic; antiinflammatory;

XX vulnary; gynaecological; antiangiogenic; hyperproliferative disease;

XX autoimmune disease; diabetes mellitus; multiple sclerosis;

XX rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;

XX endometriosis; angiogenesis.

XX Homo sapiens.

OS WO2003083102-A2.

XX 09-OCT-2003.

XX 19-MAR-2003; 2003WO-CA000393.

XX 28-MAR-2002; 2002US-0368859P.

PR (KINE-) KINETEK PHARM INC.

PA Delaney AD;

PI WPI; 2003-902934/82.

XX N-PSDB; ADD89794.

XX New nucleic acids encoding cancer associated phosphatases, useful as

PT targets for screening pharmaceutical agents that inhibit the growth of

PT tumor cells, or for diagnosing and treating cancer, inflammation or

PT autoimmune disease.

XX Claim 1; SEQ ID NO 10; 63pp; English.

XX The present invention describes an isolated cancer associated phosphatase

CC nucleic acid. Also described: (1) a method of screening for biologically

CC active agents that modulate a cancer associated phosphatase function; (2)

CC a method for the diagnosis of cancer; (3) a method for inhibiting the

CC growth of a cancer cell; (4) methods of screening for targets of a cancer

CC associated phosphatase, where the targets are associated with signal

CC transduction in cancer cells; (5) a compound (C) for the treatment of a

CC tumour; (6) a composition for the treatment of a tumour comprising a

CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and

CC (8) a method for visualising a tumour in a patient. A cancer associated

CC phosphatase of the present invention has cytostatic, immunosuppressive,

CC antidiabetic, neuroprotective, antirheumatic, antiarthritic,

CC antipsoriatic, antiarteriosclerotic, antiinflammatory, vulnary,

CC gynaecological and antiangiogenic activities. The cancer associated

CC phosphatases and nucleic acids encoding the proteins are useful for

CC visualising tumours in patients or diagnosing and treating cancer, e.g.

CC pancreas, lung, ovarian, liver or colon cancer. The polypeptides and

CC nucleic acids may also be used for treating hyperproliferative diseases,

CC such as autoimmune disease, diabetes mellitus, multiple sclerosis,

CC rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring,

CC endometriosis or angiogenesis, determining the effectiveness of drugs,

CC determining patient prognosis, or as targets for screening pharmaceutical

CC agents that inhibit the growth or metastasis of tumour cells. The present

CC sequence represents the human cancer associated phosphatase

CC DKFP566K0524, which is used in the exemplification of the present

XX invention.

SQ Sequence 398 AA;

Query Match 4.7%; Score 19; DB 7; Length 398;

Best Local Similarity 100.0%; Pred. No. 3e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 KNYRDILPYDSTRVPLGK 210

Db 164 KNYRDILPYDSTRVPLGK 182

RESULT 11

ADD89123

ID ADD89123 standard; protein; 409 AA.

XX AC ADD89123;

XX 29-JAN-2004 (first entry)

DE Novel protein-related contig polypeptide sequence #189.

XX novel gene; novel protein; tissue marker; molecular weight marker;

XX chromosome marker; genetic disorder; contig.

XX Unidentified.

OS WO2003054152-A2.

XX 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 12-APR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.

PR 22-APR-2002; 2002US-0372615P.

PR 24-APR-2002; 2002US-00128558.

XX (HYSE-) HYSEQ INC.

PA Tang Y, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma I, Wang D, Chen R, Xu C, Boyle BJ;

XX WPI; 2003-569235/53.

XX New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

XX Disclosure; SEQ ID NO 2667; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel

CC proteins. The DNA and protein sequences of the invention are useful as:

CC markers for tissues in which the corresponding protein is preferentially

CC expressed; as molecular weight markers on gels; as chromosome markers or

CC tags; to identify chromosomes or to map related gene positions; and to

CC compare with endogenous DNA sequences in patients to identify potential

CC genetic disorders. The present amino acid sequence was used in the

CC exemplification of the invention.

XX Sequence 409 AA;

Query Match 4.7%; Score 19; DB 7; Length 409;

Best Local Similarity 100.0%; Pred. No. 3.1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 KNYRDILPYDSTRVPLGK 210

Db 175 KNYRDILPYDSTRVPLGK 193

CC useful in gene therapy and for creating transgenic animals to model human  
 CC disease. The present sequence is human KPP protein

XX  
 SQ Sequence 412 AA;

Query Match 4.7%; Score 19; DB 6; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210  
 |||||  
 DB 186 KNYRDILPYDSTRVPLGK 204

## RESULT 13

AAE14454  
 ID AAE14454 standard; protein; 420 AA.

XX AAE14454;

AC AAE14454;

XX 26-MAR-2002 (first entry)

XX Human protein phosphatase-4.

DE Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;

KW neurological disorder; developmental disorder; Alzheimer's disease;

KW cell proliferative disorder; Huntington's disease; arteriosclerosis;

KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;

KW leukaemia; transgenic animal; gene therapy.

XX Homo sapiens.

XX Key

FT Region

FT Active-site

FT site"

FT Region

FT Domain

FT WO200196546-A2.

PN 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019442.

XX 16-JUN-2000; 2000US-0212447P.

PR 22-JUN-2000; 2000US-0213745P.

PR 29-JUN-2000; 2000US-0215210P.

PR 06-JUL-2000; 2000US-0216529P.

PR 12-JUL-2000; 2000US-0218080P.

PR 21-JUL-2000; 2000US-0220117P.

XX (INCY-) INCYTE GENOMICS INC.

XX Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;

XX Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;

XX Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;

XX Tribouley CM, Walla NK, Yang J, Rao MG, Yue H;

XX WPI; 2002-090206/12.

XX N-PSDB; AAD24022.

XX Novel polypeptide, useful for diagnosing, treating or preventing

XX disorders of growth and development, immune system, neurological and cell

XX proliferation diseases, comprises cancer protein phosphatase

XX polypeptides.

XX Claim 1; Page 105-106; 116pp; English.

XX

## RESULT 12

AAE37996

ID AAE37996 standard; protein; 412 AA.

XX AAE37996;

XX 06-NOV-2003 (first entry)

XX Human kinase and phosphatase (KPP-41) protein.

DE Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;

KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;

KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;

KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;

KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;

KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;

KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;

KW neutropenic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;

KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;

KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;

KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2001; 2001US-0340235P.

PR 19-DEC-2001; 2001US-0343007P.

PR 21-DEC-2001; 2001US-0343546P.

PR 04-FEB-2002; 2002US-0356388P.

PR 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;

XX Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;

XX Baughn MR, Chawla NK, Lehr-Nason PM, Khare R, Lee S, Hawkins PR;

XX Becha SD, Lee SY, Sprague WM, Zebarjadian Y;

XX WPI; 2003-532894/50.

XX N-PSDB; AAD57368.

XX New human kinases and phosphatases and polynucleotides, useful for

XX diagnosing, treating or preventing autoimmune or inflammatory disorders

XX (e.g. AIDS, allergy or anaemia), multiple sclerosis, osteoarthritis,

XX cancer or hepatitis.

XX Claim 1; Page 243-244; 282pp; English.

XX The invention relates to an isolated polypeptide, which is a human kinase

XX and phosphatase (KPP). KPP agonists and antagonists are useful for

XX diagnosing, treating or preventing disorders associated with aberrant

XX expression of KPP, particularly cell proliferative disorders (e.g.

XX arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal

XX nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary

XX thrombocytopenia or cancer), developmental disorders (eg. renal tubular

XX acidosis, anaemia or mental retardation), neurological disorders (e.g.

XX Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/

XX inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,

XX allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's

XX disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,

XX gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,

XX multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's

XX syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,

XX bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP

XX is useful in assessing the effects of exogenous compounds on the

XX expression of nucleic acids and kinases and phosphatases. KPP gene is

CC The present sequence is human protein phosphatase (PP)-4. PP  
 CC polynucleotide and polypeptide are useful in the diagnosis, treatment and  
 CC prevention of immune system disorders, neurological disorders,  
 CC developmental disorders and cell proliferative disorders. Examples of  
 CC immune system disorders include acquired immune deficiency syndrome  
 CC (AIDS), severe combined immunodeficiency disease (SCID), adult  
 CC respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,  
 CC emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple  
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic  
 CC sclerosis, trauma; neurological disorders include Alzheimer's disease,  
 CC Huntington's disease, dementia, epilepsy, Parkinson's disease, mental  
 CC retardation and other developmental disorders of central nervous system  
 CC such as Down's syndrome, cerebral palsy, periodic paralysis, mental  
 CC disorders including mood, anxiety, and schizophrenic disorders, seasonal  
 CC affective disorder such as akathisia, amnesia, catatonia, dyskinesia;  
 CC developmental disorders include e.g. renal tubular acidosis, Duchenne and  
 CC Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell  
 CC proliferative disorders include e.g. actinic keratosis, arteriosclerosis,  
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer  
 CC including adenocarcinoma, leukaemia. The polypeptide and polynucleotide  
 CC are further useful for analysing proteome of a tissue or a cell type, for  
 CC screening an agonist/antagonist, a compound that specifically binds to it  
 CC or its modulator. The polynucleotide is useful for creating knockin  
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model  
 CC human disease, for generating a transcript image of a tissue or cell  
 CC type, which represents the global pattern of gene expression by a  
 CC particular tissue or cell type  
 CC  
 CC Sequence 420 AA;

Query Match 4.7%; Score 19; DB 5; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210  
 DB 186 KNYRDILPYDSTRVPLGK 204

RESULT 14  
 ADE08106  
 ID ADE08106 standard; protein; 508 AA.  
 AC ADE08106;

XX 29-JAN-2004 (first entry)  
 XX Novel protein (useful for identifying genetic disorders) #261.  
 XX novel gene; novel protein; tissue marker; molecular weight marker;  
 XX chromosome marker; genetic disorder.

XX Unidentified.  
 XX WO2003054152-A2.  
 XX 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.  
 XX 10-DEC-2001; 2001US-0339739P.  
 XX 11-DEC-2001; 2001US-0339453P.  
 XX 14-MAR-2002; 2002US-0365091P.  
 XX 14-MAR-2002; 2002US-0365384P.  
 XX 12-APR-2002; 2002US-0372381P.  
 XX 12-APR-2002; 2002US-0372615P.  
 XX 22-APR-2002; 2002US-00128558.  
 XX 24-APR-2002; 2002US-0376045P.  
 XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;  
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;  
 XX WPI; 2003-569235/53.  
 DR N-PSDB; ADE07195.

XX New polynucleotides, useful for expressing recombinant proteins for  
 PT analysis, characterization or therapeutic use, or as markers for tissues  
 PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1172; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence represents a protein  
 CC of the invention.

XX Sequence 508 AA;

Query Match 4.7%; Score 19; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210  
 DB 274 KNYRDILPYDSTRVPLGK 292

RESULT 15  
 ABG06042  
 ID ABG06042 standard; protein; 561 AA.

XX ABG06042;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #6033.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS70229.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensic, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX Claim 20; SEQ ID NO 36401; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 561 AA;

Query Match 4.7%; Score 19; DB 4; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 KNYRDILPYDSTRVPLGK 210  
 DB 327 KNYRDILPYDSTRVPLGK 345

RESULT 16  
 AAW67441  
 ID AAW67441 standard; protein; 272 AA.

XX AC AAW67441;

XX DT 25-MAR-2003 (revised)

XX DT 02-MAR-1999 (first entry)

XX DE N-terminus of the human protein tyrosine phosphatase D1.

XX KW Human; protein tyrosine phosphatase; skeletal muscle; hybridisation;  
 KW Glycoprotein; probe.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 101 /note= "encoded byv NGA"

XX FT Misc-difference 102 /note= "encoded by NNG"

XX FT Misc-difference 157 /note= "encoded by CNN"

XX FT /note= "encoded by CNN"

XX PN US5831009-A.

XX XX 03-NOV-1998.

XX PD 22-MAY-1995; 95US-00446345.

XX XX 05-AUG-1992; 92US-00923740.

XX PR 27-APR-1994; 94US-00234440.

XX XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX PI Moller NPH, Moller KB, Ullrich A;

XX DR WPI; 1998-609316/51.

XX DR N-PSDB; AAW34371.

XX XX Protein tyrosine phosphatase D1 - useful in screening assays for e.g.

PT agonists or antagonists.  
 XX XX Example 2; Fig 4; 61pp; English.  
 XX CC This sequence represent the N-terminal amino acid sequence of the human  
 CC protein tyrosine phosphatase D1 (PTP-D1). The coding fragment was  
 CC amplified by PCR. The complete gene sequence (AAV34368) was isolated from  
 CC a human skeletal muscle cDNA library. The phosphatase is used e.g. in a  
 CC hybridisation assay for detecting a nucleic acid encoding a normal or  
 CC mutant PTP-D protein or glycoprotein in a cell or subject, using a  
 CC nucleic acid comprising at least part of a normal or mutant PTP-D protein  
 CC or glycoprotein as a probe; or a screening assay for a compound capable  
 CC of binding to a PTP-D protein or glycoprotein, using a PTP-D protein or  
 CC glycoprotein or the compound-binding portion of it attached to a solid  
 CC support. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 272 AA;

Query Match 3.7%; Score 15; DB 2; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGV 368

DB 201 PLLVHCSAGVGRGV 215

XX AC AAY34161;

XX DT 09-NOV-1999 (first entry)

XX DE Human PTP-D1 protein sequence fragment.

XX KW PTP-D1; human; protein tyrosine phosphatase; neoplastic formation;  
 KW PTPase; growth factor signal transduction; cell cycle progression;  
 KW cancer; diabetes; cellular phosphotyrosine metabolism.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 101 /label= unknown  
 /note= "encoded by NGA"

XX FT Misc-difference 102 /label= unknown  
 /note= "encoded by NNG"

XX FT Misc-difference 157 /label= unknown  
 /note= "encoded by CNN"

XX FT /note= "encoded by CNN"

XX PN US5955592-A.

XX XX 21-SEP-1999.

XX PD 27-APR-1994; 94US-00234440.

XX XX 05-AUG-1992; 92US-00923740.

XX PR (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX PI Moller NPH, Moller KB, Ullrich A;

XX DR WPI; 1999-539599/45.

XX DR N-PSDB; AAZ11227.

XX XX Nucleic acids encoding protein phosphotyrosine phosphatase PTP-D1 useful  
 for identification of PTP-D1 modulators.

XX XX Example 2; Fig 4; 63pp; English.

XX This sequence represents a partial fragment of the protein tyrosine  
 CC phosphatase of the invention, designated PTP-D1. The new PTP proteins are  
 CC a subfamily of protein tyrosine phosphatases (PTPases) involved with  
 CC growth factor signal transduction, cell cycle progression, and neoplastic  
 CC formation. The DNA sequence may be used in the recombinant production of  
 CC PTP-D1 according to standard DNA methodology. The protein expressed may  
 CC then be used in assays to identify modulators of its enzymatic activity  
 CC and in the production of antibodies. The nucleic acids may also be used  
 CC in assays to detect and quantify expression of PTP-D1 in samples. Methods  
 CC identifying normal or mutant PTP-D genes, or for measuring amount or  
 CC activity of the protein can serve as methods for identifying  
 CC susceptibility to cancer, diabetes, or other disorders associated with  
 CC alterations in cellular phosphotyrosine metabolism

XX SQ Sequence 272 AA;

Query Match 3.7%; Score 15; DB 2; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGTG 368  
 DB 201 PLLVHCSAGVGRGTG 215  
 |||||

# RESULT 18

AAW25567  
 ID AAW25567 standard; protein; 1105 AA.

XX AC AAW25567;

DT 16-OCT-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:1082.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema;  
 KW dermatological; antiallergic; antiaslthmatic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder.

XX OS Homo sapiens.

XX FN WO200153455-A2.

XX PD 26-JUL-2001.

XX PF 22-DEC-2000; 2000WO-US035017.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-457603/49.

XX DR N-PSDB; AAH99508.

XX Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX PS Claim 20; Page 219; 1217pp; English.  
 XX CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 CC AAM25963. The proteins can have activities based on the tissues and cells  
 CC they are expressed in, such as: antiinflammatory; antirheumatic;  
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;  
 CC antilucer; osteopathic; dermatological; antiallergic; antiaslthmatic;  
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antisense therapy and vaccine  
 CC production. The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders

XX SQ Sequence 1105 AA;

Query Match 3.7%; Score 15; DB 4; Length 1105;

Best Local Similarity 100.0%; Pred. No. 9.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGTG 368

DB 1015 PLLVHCSAGVGRGTG 1029  
 |||||

# RESULT 19

AAW67438  
 ID AAW67438 standard; protein; 1174 AA.

XX AC AAW67438;

XX DT 25-MAR-2003 (revised)

XX DT 02-MAR-1999 (first entry)

XX DE Human protein tyrosine phosphatase D1 protein.

XX KW Human; protein tyrosine phosphatase; skeletal muscle; hybridisation;  
 KW glycoprotein; probe.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 24..339

FT Binding-site /note= "ezrin-like domain"

FT Binding-site 158..161

FT Binding-site /note= "SH2 binding motif"

FT Binding-site 207..210

FT Binding-site /note= "SH2 binding motif"

FT Modified-site 217..220

FT Modified-site /note= "SH2 binding motif"

FT Modified-site 336..338

FT Modified-site /note= "PYX motif, putative site of Tyr phosphorylation"

FT Modified-site 354..356

FT Modified-site /note= "PYX motif, putative site of Tyr phosphorylation"

FT Modified-site 408..410

FT Modified-site /note= "PYX motif, putative site of Tyr phosphorylation"

FT Modified-site 523..525

FT Modified-site /note= "PYX motif, putative site of Tyr phosphorylation"

FT Modified-site 525..527

FT Modified-site /note= "PYX motif, putative site of Tyr phosphorylation"

FT Binding-site 565..574

FT Binding-site /note= "SH3 binding domain"



FT Modified-site 568..570  
 FT /note= "PYX motif, putative site of Tyr phosphorylation"  
 FT Region 712..722  
 FT /note= "acidic stretch"  
 FT Domain 921..1166  
 FT /note= "protein tyrosine phosphatase domain"  
 XX US5831009-A.  
 XX 03-NOV-1998.  
 XX 22-MAY-1995; 95US-00446345.  
 XX 05-AUG-1992; 92US-00923740.  
 XX 27-APR-1994; 94US-00234440.  
 XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX Moller NPH, Moller KB, Ullrich A;  
 XX WPI; 1998-609316/51.  
 XX N-PSDB; AAV34368.  
 XX Protein tyrosine phosphatase D1 - useful in screening assays for e.g.  
 XX agonists or antagonists.  
 XX Claim 1; Fig 5A-J; 6lpp; English.  
 XX This is the sequence of the complete human protein tyrosine phosphatase  
 CC D1 (PTP-D1). The coding sequence was isolated from a human skeletal  
 CC muscle cDNA library. The phosphatase is used e.g. in a hybridisation  
 CC assay for detecting a nucleic acid encoding a normal or mutant PTP-D  
 CC protein or glycoprotein in a cell or subject, using a nucleic acid  
 CC comprising at least part of a normal or mutant PTP-D protein or  
 CC glycoprotein as a probe; or a screening assay for a compound capable of  
 CC binding to a PTP-D protein or glycoprotein, using a PTP-D protein or  
 CC glycoprotein or the compound-binding portion of it attached to a solid  
 CC support. (Updated on 25-MAR-2003 to correct PR field.)  
 XX Sequence 1174 AA;  
 SQ Query Match 3.7%; Score 15; DB 2; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 354 PLLVHCSAGVGRGTG 368  
 Db |||||  
 1103 PLLVHCSAGVGRGTG 1117  
 RESULT 20  
 AAY34158  
 ID AAY34158 standard; protein; 1174 AA.  
 AC AAY34158;  
 XX 09-NOV-1999 (first entry)  
 XX Human protein tyrosine phosphatase, PTP-D1, protein sequence.  
 XX PTP-D1; human; protein tyrosine phosphatase; neoplastic formation;  
 KW PTPase; growth factor signal transduction; cell cycle progression;  
 KW cancer; diabetes; cellular phosphotyrosine metabolism.  
 XX Homo sapiens.  
 OS US5955592-A.  
 XX 21-SEP-1999.  
 XX 27-APR-1994; 94US-00234440.  
 XX 05-AUG-1992; 92US-00923740.

XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX Moller NPH, Moller KB, Ullrich A;  
 XX WPI; 1999-539599/45.  
 XX N-PSDB; AAZ11221.  
 XX Nucleic acids encoding protein phosphotyrosine phosphatase PTP-D1 useful  
 PT for identification of PTP-D1 modulators.  
 XX Claim 1; Fig 5; 63pp; English.  
 XX This sequence is the protein tyrosine phosphatase of the invention,  
 CC designated PTP-D1. The new PTP proteins are a subfamily of protein  
 CC tyrosine phosphatases (PTPases) involved with growth factor signal  
 CC transduction, cell cycle progression, and neoplastic formation. The DNA  
 CC sequence may be used in the recombinant production of PTP-D1 according to  
 CC standard DNA methodology. The protein expressed may then be used in  
 CC assays to identify modulators of its enzymatic activity and in the  
 CC production of antibodies. The nucleic acids may also be used in assays to  
 CC detect and quantify expression of PTP-D1 in samples. Methods identifying  
 CC normal or mutant PTP-D genes, or for measuring amount or activity of the  
 CC protein can serve as methods for identifying susceptibility to cancer,  
 CC diabetes, or other disorders associated with alterations in cellular  
 CC phosphotyrosine metabolism  
 XX Sequence 1174 AA;  
 SQ Query Match 3.7%; Score 15; DB 2; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 354 PLLVHCSAGVGRGTG 368  
 Db |||||  
 1103 PLLVHCSAGVGRGTG 1117  
 RESULT 21  
 ADD45494  
 ID ADD45494 standard; protein; 1174 AA.  
 AC ADD45494;  
 XX 29-JAN-2004 (first entry)  
 XX Human Protein Q16825, SEQ ID NO 11128.  
 XX Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX Homo sapiens.  
 OS WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GERO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 WPI; 2003-268312/26.  
 DR GENBANK; Q16825.  
 XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1174 AA;

Query Match 3.7%; Score 15; DB 7; Length 1174;

Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGV 368

Db 1103 PLLVHCSAGVGRGV 1117

RESULT 23

ADBE3529  
 ID ADBE3529 standard; protein; 1175 AA.

AC ADBE3529;

DT 29-JAN-2004 (first entry)

DB Rat Protein Q62728, SEQ ID NO 11126.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

PN WO2003016475-A2.

PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENEANK; Q62728.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1175 AA;

Query Match 3.7%; Score 15; DB 7; Length 1175;

Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGRGV 368

Db 1104 PLLVHCSAGVGRGV 1118

RESULT 23

ADBE1029  
 ID ADBE1029 standard; protein; 1175 AA.

AC ADBE1029;

DT 29-JAN-2004 (first entry)

DE Rat Protein Q62728, SEQ ID NO 6943.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

PN WO2003016475-A2.

PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI: 2003-268312/26.  
 DR GENBANK; Q62728.  
 DR

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX

PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

SQ Sequence 1175 AA;

Query Match 3.7%; Score 15; DB 7; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGTGV 368  
 |||||  
 Db 1104 PLLVHCSAGVGTGV 1118

RESULT 24  
 ADE61033  
 ID ADE61033 standard; protein; 1175 AA.

XX ADE61033;

XX 29-JAN-2004 (first entry)

DE Rat Protein Q62728, SEQ ID NO 6947.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US25765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-0333347P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI: 2003-268312/26.

DR GENBANK; Q62728.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX

PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

SQ Sequence 1175 AA;

Query Match 3.7%; Score 15; DB 7; Length 1175;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 PLLVHCSAGVGTGV 368  
 |||||  
 Db 1104 PLLVHCSAGVGTGV 1118

RESULT 25  
 AAR60876

ID AAR60876 standard; protein; 176 AA.

XX AAR60876;

XX 25-MAR-2003 (revised)

DT 26-JUN-1995 (first entry)

XX Product of the partial PCR fragment of PTP-S31.

XX Protein tyrosine phosphatase; cancer; diabetes.

XX Homo sapiens.

XX WO9421800-A2.

XX 29-SEP-1994.

XX 23-MAR-1994; 94MO-EP000909.  
 XX  
 XX 23-MAR-1993; 93US-00036210.  
 XX

XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX

XX Moller NPH, Moller KB, Ullrich A;  
 XX

XX WPI; 1994-317020/39.  
 XX

XX N-PSDB; AAQ73785.  
 XX

XX New protein tyrosine phosphatase PTP-531 - is used to develop prods. for  
 PT treating or preventing disease associated with abnormal PTP-531, e.g.  
 PT cancer or diabetes.  
 XX

XX Claim 6; Fig 5; 116pp; English.  
 XX

XX The sequence is that of a partial fragment of a new protein tyrosine  
 CC phosphatase PTP-531 that was isolated from RNA from human skeletal muscle.  
 CC Such DNA can be used to treat cancer and diabetes. See also AAR60875-9.  
 CC  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX

XX Sequence 176 AA;  
 SQ

Query Match 3.5%; Score 14; DB 2; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVPI 370  
 |||||

Db 79 VHCSAGVGRGTGVPI 92

RESULT 26

AAB59389

ID AAB59389 standard; protein; 245 AA.

XX  
 AC AAB59389;

XX 21-MAR-2001 (first entry)  
 DT

XX Human protein tyrosine phosphatase #17.  
 DE

XX Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
 KW substrate trapping.  
 XX

XX Homo sapiens.  
 OS

XX WO200075339-A1.  
 PN

XX 14-DEC-2000.  
 PD

XX 24-MAY-2000; 2000WO-US014211.  
 PF

XX 03-JUN-1999; 99US-0137319P.  
 PR

XX 16-JUN-1999; 99US-00334575.  
 XX

XX (COLD-) COLD SPRING HARBOR LAB.  
 PA

XX Tonks NK, Zhang S;  
 PI

XX WPI; 2001-080598/09.  
 DR

XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
 PT which the wild type PTP catalytic domain invariant aspartate is replaced  
 PT with an unphosphorylated amino acid, useful in gene therapy.  
 XX

XX Disclosure; Fig 1; 109pp; English.  
 PS

XX The present invention provides substrate trapping mutant protein tyrosine  
 CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
 CC phosphorylated proteins and to screen for modulators capable of altering

CC the binding of protein tyrosine phosphatases to their substrate. These  
 CC may be used in disease diagnosis and treatment  
 XX  
 SQ Sequence 245 AA;

Query Match 3.5%; Score 14; DB 4; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVPI 370  
 |||||

Db 183 VHCSAGVGRGTGVPI 196

RESULT 27

AAG78287

ID AAG78287 standard; protein; 294 AA.

XX  
 AC AAG78287;

XX 19-DEC-2001 (first entry)  
 DT

XX Human BCA-D2.  
 DE

XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;  
 KW dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;  
 KW yeast.  
 XX

XX Homo sapiens.  
 OS

XX WO200161031-A2.  
 PN

XX 23-AUG-2001.  
 PD

XX 13-FEB-2001; 2001WO-US005180.  
 PF

XX 14-FEB-2000; 2000US-0181769P.  
 PR

XX (CEPT-) CEPTYR INC.  
 PA

XX Flint AJ, Cool DB;  
 PI

XX WPI; 2001-570570/64.  
 DR

XX Screening assays to identify agents that alter protein tyrosine  
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic  
 PT dephosphorylation of phosphotyrosine peptide substrates.  
 XX

XX Disclosure; Fig 1; 79pp; English.  
 PS

XX The invention relates to identifying agents which alter the interaction  
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine  
 CC phosphorylated polypeptide using fluorescence energy signals. The methods  
 CC are useful for performing screening assay to identify agents that alter  
 CC PTP binding to and PTP-mediated catalytic dephosphorylation of  
 CC phosphotyrosine peptide substrates. The present sequence is that of a  
 CC catalytic domain of a PTP for comparison with human PTP1B (AAG78262)  
 XX

SQ Sequence 294 AA;

Query Match 3.5%; Score 14; DB 4; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVPI 370  
 |||||

Db 183 VHCSAGVGRGTGVPI 196

RESULT 28

AAR60877

ID AAR60877 standard; protein; 322 AA.

XX

AC AAR60877;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-JUN-1995 (first entry)  
 XX  
 DE Product of the partial PCR fragment of PTP-S31.  
 XX  
 KW Protein tyrosine phosphatase; cancer; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9421800-A2.  
 XX  
 PD 29-SEP-1994.  
 XX  
 PF 23-MAR-1994; 94WO-EP000909.  
 XX  
 PR 23-MAR-1993; 93US-00036210.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Moller NPH, Moller KB, Ullrich A;  
 XX  
 DR WPI; 1994-317020/39.  
 DR N-PSDB; AAQ73786.  
 XX  
 PT New protein tyrosine phosphatase PTP-S31 - is used to develop prods. for  
 PT treating or preventing disease associated with abnormal PTP-S31, e.g.  
 PT cancer or diabetes.  
 XX  
 PS Claim 6; Fig 6; 116pp; English.  
 XX  
 CC The sequence is that of a partial fragment of a new protein tyrosine  
 CC phosphatase PTP-S31 that was isolated from RNA from human skeletal muscle.  
 CC Such DNA can be used to treat cancer and diabetes. See also AAR60875-9.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 322 AA;  
 Query Match 3.5%; Score 14; DB 2; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGRGTGVFI 370  
 DB 221 VHCSAGVGRGTGVFI 234  
 RESULT 29  
 ID AAR56372  
 AC AAR56372 standard; protein; 442 AA.  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human prostate cancer antigen protein sequence SEQ ID NO:950.  
 XX  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055174-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005988.  
 XX

PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587513/55.  
 DR N-PSDB; AAF15575.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate cancer  
 PT antigens, useful for treatment, prevention, and diagnosis of disorders  
 PT such as prostate cancer.  
 XX  
 PS Claim 11; Page 1389-1390; 2338pp; English.  
 XX  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF1506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 442 AA;  
 Query Match 3.5%; Score 14; DB 3; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCSAGVGRGTGVFI 370  
 DB 372 VHCSAGVGRGTGVFI 385  
 RESULT 30  
 ID AAY81783  
 AC AAY81783 standard; protein; 607 AA.  
 XX  
 DT 07-JUN-2000 (first entry)  
 XX  
 DE Human protein tyrosine phosphatase specific antibody protein sequence.  
 XX  
 KW Human; protein tyrosine phosphatase; antibody; intracellular domain; IAR;  
 KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;  
 KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;  
 KW heart disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200002922-A1.  
 XX  
 PD 20-JAN-2000.  
 XX  
 PF 06-JUL-1999; 99WO-JP003656.  
 XX  
 PR 10-JUL-1998; 98WO-JP003120.  
 XX  
 PA (FUSO ) FUSO PHARM IND LTD.  
 XX  
 PI Yamamoto H, Tsujikawa K, Uchino Y;  
 XX  
 DR WPI; 2000-182215/16.  
 DR N-PSDB; AAZ91907.  
 XX



DT 24-OCT-2001 (first entry)  
 XX Human novel protein #250.  
 DE  
 XX  
 XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
 KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
 KW anticonvulsant; antiarthritic; cerabroprotective; antifungal; antitvital;  
 KW antibacterial; antiatheric; dermatological; haemostatic; antisthmatic;  
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200155437-A2.  
 XX  
 XX PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US002623.  
 XX  
 XX 25-JAN-2000; 2000US-00491404.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Drmanac RT;  
 XX  
 XX WPI; 2001-451939/48.  
 XX  
 XX N-PSDB; AAS22684.  
 XX  
 PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
 PT nervous system disorders, and for regenerating bone and cartilage.  
 XX  
 XX Example 4; Page 792-793; 894pp; English.  
 XX  
 CC The invention relates to polynucleotides encoding novel human proteins or  
 CC their active domains. The polypeptides, polynucleotides and antibodies  
 CC raised against the polypeptides are used in a method of treatment of a  
 CC mammal and prevention of disorders caused by the aberrant protein  
 CC expression or activity. The polypeptides can be used as molecular weight  
 CC markers, food supplements, and in antibody production. The polypeptides  
 CC are used to identify compounds which bind to the polypeptides.  
 CC Polynucleotides of the invention are used as probes and primers, for  
 CC sequencing, for chromosome or gene mapping, in the production of  
 CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene  
 CC therapy. Polypeptides of the invention can be used to target drugs to a  
 CC tumour, in assays to determine biological activity, to raise  
 CC antibodies/elicite an immune response, to determine quantitative protein  
 CC levels, as tissue markers, and to isolate receptors or ligands.  
 CC Polypeptides of the invention may also be useful in treating platelet  
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
 CC the proliferation, differentiation and survival of stem cells, as a  
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-  
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory  
 CC diseases, nervous system disorders, and infection. The present sequence  
 CC represents a protein of the invention  
 XX  
 XX SQ Sequence 647 AA;  
 Query Match 3.5%; Score 14; DB 4; Length 647;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGTGVFI 370  
 |||||  
 DB 577 VHCAGVGTGVFI 590  
 RESULT 34  
 AAR75201

ID AAR75201 standard; protein; 1291 AA.  
 XX  
 AC AAR75201;  
 XX  
 DT 10-MAY-1996 (first entry)  
 XX  
 XX Tyrosine phosphatase MPTP-delta.  
 DE  
 DE Tyrosine phosphatase MPTP-delta.  
 KW Tyrosine phosphatase MPTP-delta; murine; brain tissue;  
 KW glutathione-S-transferase; fusion protein; E. coli; differentiation;  
 KW activation; information transmission; nervous system; immune system;  
 KW carcinogenesis.  
 XX  
 XX Mus musculus domesticus.  
 OS  
 XX JP07236487-A.  
 XX  
 XX 12-SEP-1995.  
 XX  
 XX 28-FEB-1994; 94JP-00054726.  
 PF  
 XX 28-FEB-1994; 94JP-00054726.  
 PR  
 XX (TOKS-) TOKYO SHINKAI KAGAKU SOGO KENKYUSHO ZH.  
 XX  
 XX WPI; 1995-347455/45.  
 XX  
 XX N-PSDB; AAQ94311.  
 DR  
 XX DNA encoding tyrosine phosphatase MPTP delta - useful for elucidation of  
 PT signal transmission mechanisms.  
 PT  
 XX Claim 1; Page 5-11; 14pp; Japanese.  
 PS  
 XX This sequence represents murine tyrosine phosphatase MPTP-delta. The cDNA  
 CC sequence encoding this protein was isolated from murine brain tissue and  
 CC was cloned, for expression, into the downstream region of a glutathione-S-  
 CC transferase sequence and expressed as a fusion protein in E. coli. MPTP-  
 CC delta proteins regulate differentiation and activation of cells. This  
 CC sequence can be used in the elucidation of the molecular mechanism for  
 CC information transmission in cells, regulation mechanisms in the nervous  
 CC system or immune system, or in the mechanism of carcinogenesis  
 XX  
 XX SQ Sequence 1291 AA;  
 Query Match 3.5%; Score 14; DB 2; Length 1291;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGTGVFI 370  
 |||||  
 DB 1221 VHCAGVGTGVFI 1234  
 RESULT 35  
 ABB57380  
 ID ABB57380 standard; protein; 1495 AA.  
 XX  
 AC ABB57380;  
 XX  
 XX 07-AUG-2003 (revised)  
 DT  
 DT 08-MAR-2002 (first entry)  
 XX  
 XX Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 12.  
 DE  
 XX Rat; heart; cardiant; myocardial necrosis; cardiac hypertrophy;  
 KW cardiac insufficiency.  
 KW  
 XX Rattus norvegicus.  
 OS  
 XX WO200183705-A1.  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX

2F 27-APR-2001; 2001WO-JP003700.

XX PR 27-APR-2000; 2000JP-00126741.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Yamada Y, Sekine S, Kikuchi Y, Sakurada K;

XX DR WPI; 2002-075160/10.

XX DR N-PSDB; AB199920.

XX PT Genes having differential expression in fetal and adult heart tissue

XX PT useful for screening potential drugs for promoting repair of damage

XX PT caused by myocardial necrosis.

XX PS Claim 53; Page 110-116; 171pp; Japanese.

XX CC The invention relates to gene sequences (AB199915-AB199934) having

XX CC modified expression in fetal heart tissue as compared to adult heart

XX CC tissue and the encoded proteins (AB57375-AB57392). The genes have

XX CC radiant activity and may be useful in the promotion of the repair of

XX CC damage to heart tissue caused by myocardial necrosis. The gene sequences

XX CC are useful for screening potential compounds for the ability to influence

XX CC disease associated with myocardial necrosis. Drugs identified by the

XX CC screening methods may be used to treat and prevent disease with which

XX CC myocardial necrosis is associated, such as cardiac hypertrophy and

XX CC cardiac insufficiency. Diagnosis of diseases such as those above is also

XX CC disclosed. (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 1495 AA;

Query Match 3.5%; Score 14; DB 5; Length 1495;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVPI 370

Db 1426 VHCSAGVGRGTGVPI 1439

RESULT 36

ID ADE57115

XX AC ADE57115 standard; protein; 1496 AA.

XX AC ADE57115;

DT 29-JAN-2004 (first entry)

DE Rat Protein L19180, SEQ ID NO 2975.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX DR GENBANK; L19180.

XX

PT

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PS

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CC

PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX

XX

PS Claim 1; Page; 1017pp; English.

XX

XX

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1496 AA;

Query Match 3.5%; Score 14; DB 7; Length 1496;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVPI 370

Db 1426 VHCSAGVGRGTGVPI 1439

RESULT 37

AD57119

ID ADE57119 standard; protein; 1496 AA.

XX AC ADE57119;

XX

DT 29-JAN-2004 (first entry)

DE Rat Protein L19180, SEQ ID NO 2979.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort X, Costigan M;



XX WPI; 2003-268312/26.  
 DR GENBANK; L19180.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1496 AA;

Query Match 3.5%; Score 14; DB 7; Length 1496;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 Db 1426 VHCAGVGRGTGVFI 1439

RESULT 38  
 ADD47013  
 ID ADD47013 standard; protein; 1496 AA.

XX ADD47013;

XX 29-JAN-2004 (first entry)

XX Rat Protein L19180, SEQ ID NO 12699.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP.  
 PA (PARB ) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; L19180.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1496 AA;

Query Match 3.5%; Score 14; DB 7; Length 1496;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 Db 1426 VHCAGVGRGTGVFI 1439

RESULT 39  
 ADD47017  
 ID ADD47017 standard; protein; 1496 AA.

XX ADD47017;

XX 29-JAN-2004 (first entry)

XX Rat Protein L19180, SEQ ID NO 12703.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;  
 DR GENEANK; L19180.

XX WPI; 2003-268312/26.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1496 AA;

Query Match 3.5%; Score 14; DB 7; Length 1496;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRTGVFI 370

Db 1426 VHCAGVGRTGVFI 1439

RESULT 40

ID AAR72858 AAR72858 standard; protein; 1501 AA.

XX AAR72858;

XX AAR72858;

XX 25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

XX Rat receptor type-protein tyrosine phosphatase sigma.

XX Receptor type tyrosine phosphatase sigma; cell; differentiation;

XX metabolism; cell cycle; behaviour; motility; contact inhibition; virus;

XX inflammation; cellular transformation; cancer; neuroblastomas; antibody;

XX detection; quantification.

XX Rattus rattus.

XX WO9509656-A1.

XX 13-APR-1995.

XX 30-SEP-1994; 94WO-US011163.

XX 01-OCT-1993; 93US-00130570.

XX (UUNY ) UNIV NEW YORK STATE.

XX Schlessinger J, Yan H;

XX WPI; 1995-155068/20.

XX N-PSDB; AAQ86902.

XX Novel, isolated receptor-type protein tyrosine phosphatase-sigma - and  
 PT encoding DNA, useful e.g. for detecting neuro-blastomas.

XX Claim 2; Fig 2; 105pp; English.

XX Ligands binding to the receptor-type protein tyrosine phosphatase sigma  
 CC (RPTP sigma) protein may be used as drugs to modulate cellular processes,  
 CC such as differentiation, metabolism and cell cycle control, and cellular  
 CC behaviour such as motility and contact inhibitions. In addition they may  
 CC affect abnormal or potentially deleterious processes such as virus-  
 CC receptor interactions, inflammation and cellular transformation to a  
 CC cancerous state. They may also be used to treat RPTP sigma related  
 CC neuronal disorders such as neuroblastomas. The DNA encoding the RPTP  
 CC sigma is useful for the diagnosis of diseases resulting from its aberrant  
 CC expression. Antibodies directed against RPTP sigma may be used in  
 CC detection and quantitative analysis. (Updated on 25-MAR-2003 to correct  
 CC PN field.)

XX Sequence 1501 AA;

Query Match 3.5%; Score 14; DB 2; Length 1501;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRTGVFI 370

Db 1431 VHCAGVGRTGVFI 1444

RESULT 41

ID AAE37971 standard; protein; 1796 AA.

XX AAE37971;

XX 06-NOV-2003 (first entry)

XX Human kinase and phosphatase (KPP-16) protein.

XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;  
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;  
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;  
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;  
 KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;  
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;  
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;  
 KW neutropenic; dermatitis; multiple sclerosis; diabetes mellitus;  
 KW allergic; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;  
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;  
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

PF 06-DEC-2002; 2002WO-US039126.  
 XX  
 XX 07-DEC-2001; 2001US-0340235P.  
 PR 19-DEC-2001; 2001US-0343007P.  
 PR 21-DEC-2001; 2001US-0343546P.  
 PR 04-FEB-2002; 2002US-0354388P.  
 PR 15-FEB-2002; 2002US-0357675P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;  
 PI Hafalia AJA, Emerling BX, Ramkumar J, Jin P, Griffin JA, Marquis JP;  
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;  
 PI Becha SD, Lee SV, Sprague WW, Zebardjadian Y;  
 XX  
 DR WPI; 2003-532894/50.  
 DR N-PSDB; AAD57343.

XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX

PS Claim 1; Page 216-220; 282pp; English.

XX The invention relates to an isolated polypeptide, which is a human kinase  
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for  
 CC diagnosing, treating or preventing disorders associated with aberrant  
 CC expression of KPP, particularly cell proliferative disorders (e.g.  
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal  
 CC nocturnal haemoglobinuria, polycythemia vera, psoriasis, primary  
 CC thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular  
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/  
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,  
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's  
 CC syndrome, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,  
 CC bacterial, rheumatoid arthritis, Sjogren's syndrome, or viral,  
 CC expression in assessing the effects of exogenous compounds on the  
 CC is useful in assessing the effects of exogenous compounds on the  
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is  
 CC useful in gene therapy and for creating transgenic animals to model human  
 CC disease. The present sequence is human KPP protein  
 XX

SQ Sequence 1796 AA;  
 Query Match 3.5%; Score 14; DB 6; Length 1796;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASGAGVGTGVFI 370  
 DB 1726 VHCASGAGVGTGVFI 1739

RESULT 42  
 ADD46989  
 ID ADD46989 standard; protein; 1863 AA.

XX ADD46989;  
 XX 29-JAN-2004 (first entry)

DE Rat Protein AAC37656, SEQ ID NO 12675.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS  
 XX WO2003016475-A2.  
 FN

XX 27-FEB-2003.  
 XX  
 XX 14-AUG-2002; 2002WO-US025765.  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.  
 PA (PARE) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.  
 DR GENBANK; AAC37656.

XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1863 AA;

Query Match 3.5%; Score 14; DB 7; Length 1863;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCASGAGVGTGVFI 370  
 DB 1793 VHCASGAGVGTGVFI 1806

RESULT 43  
 AAY81785  
 ID AAY81785 standard; protein; 1897 AA.

XX AAY81785;

XX 07-JUN-2000 (first entry)

DE Human protein tyrosine phosphatase, LAR, protein sequence.

XX Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;  
 KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;  
 FN

KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;  
 KW heart disorder.

OS Homo sapiens.

PN WO200002922-A1.

XX 20-JAN-2000.

XX 06-JUL-1999; 99WO-JP003656.

XX 10-JUL-1998; 98WO-JP003120.

XX (FUSO ) FUSO PHARM IND LTD.

PI Yamamoto H, Tsujikawa K, Uchino Y;

DR WPI; 2000-182215/16.

DR N-PSDB; AA291908.

XX Antibody for diagnosis and treatment of insulin resistance disorders and  
 PT syndrome X recognises the intracellular domains of tyrosine kinases.

PS Example 1; Page 61-77; 83pp; Japanese.

CC This sequence is the protein tyrosine phosphatase LAR. The invention  
 CC relates to an antibody specifically recognising the intracellular domains  
 CC of two or more protein tyrosine phosphatases (PTPs). The antibody is  
 CC useful for the detection and assay of PTP including novel phosphatases  
 CC generated by cloning; and diagnosis, treatment and prevention of insulin  
 CC resistance related diseases and non-insulin dependent diabetes mellitus,  
 CC syndrome X and arteriosclerosis and heart disorders

XX Sequence 1897 AA;

Query Match 3.5%; Score 14; DB 3; Length 1897;

Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370

DB 1827 VHCAGVGRGTGVFI 1840

RESULT 44

AAAY56100

ID AAAY56100 standard; protein; 1897 AA.

AC AAAY56100;

XX 17-APR-2000 (first entry)

DE LAR tyrosine phosphatase.

KW Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;  
 KW tyrosine phosphatase; antibody; thyroid cancer.

OS Homo sapiens.

PN WO9964591-A1.

XX 16-DEC-1999.

XX 07-JUN-1999; 99WO-JP003054.

XX 08-JUN-1998; 98WO-JP002542.

XX (FUSO ) FUSO PHARM IND LTD.

PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;

DR WPI; 2000-097539/08.

DR N-PSDB; AA259133.

XX Antibody recognizing the intracellular domain of the human tyrosine  
 PT phosphatase LAR.

XX Disclosure; Page 81-97; 104pp; Japanese.

XX This sequence represents the complete human leucocyte antigen related  
 CC (LAR) tyrosine phosphatase. The invention relates to the generation of an  
 CC antibody recognizing the intracellular domain of the human LAR tyrosine  
 CC phosphatase (AA56098). The antibody is used for the diagnosis and  
 CC treatment of thyroid cancer

XX Sequence 1897 AA;

Query Match 3.5%; Score 14; DB 3; Length 1897;

Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370

DB 1827 VHCAGVGRGTGVFI 1840

RESULT 45

AAAB19712

ID AAAB19712 standard; protein; 1897 AA.

XX AAAB19712;

XX 19-FEB-2001 (first entry)

DE Human protein tyrosine phosphatase PAP LAR.

KW PTP LAR; protein tyrosine phosphatase; leucocyte antigen related; human;  
 KW epithelial cell; cell migration; cell proliferation; cancer; antitumour;  
 KW metastasis; antimetastatic; wound healing; vulnery; diagnosis; therapy.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..16 /label= Signal\_peptide  
 FT Protein 17..1897 /label= Mature\_protein  
 FT Domain 37..99 /label= Immunoglobulin\_domain  
 FT Domain 139..199 /label= Immunoglobulin\_domain  
 FT Domain 236..290 /label= Immunoglobulin\_domain  
 FT Domain 309..391 /label= Fibronectin-type-III\_domain  
 FT Domain 403..490 /label= Fibronectin-type-III\_domain  
 FT Domain 502..584 /label= Fibronectin-type-III\_domain  
 FT Domain 596..686 /label= Fibronectin-type-III\_domain  
 FT Domain 698..799 /label= Fibronectin-type-III\_domain  
 FT Domain 811..894 /label= Fibronectin-type-III\_domain  
 FT Domain 905..990 /label= Fibronectin-type-III\_domain  
 FT Domain 1365..1596 /label= Protein-tyrosine\_phosphatase

XX WO2000061180-A2.

XX 19-OCT-2000.

XX 06-APR-2000; 2000WO-US009274.

PR 09-APR-1999; 99US-0128673P.

XX (PLAC ) MAX PLANCK INST.

XX Ullrich A, Muller T;

XX WPI; 2000-647399/62.

DR N-PSDB; AAB88739.

XX Treating a disease or a disorder characterized by epithelial cell  
PT migration comprises administering a pharmaceutically acceptable  
PT composition comprising PTP LAR.

XX Disclosure; Fig 9; 107pp; English.

XX The present sequence is that of human protein tyrosine phosphatase PTP  
CC LAR (leukocyte antigen related), a negative regulator of epithelial cell  
CC migration and tumour formation, for which beta-catenin is a substrate. A  
CC dysfunction of PTP LAR may lead to tumour invasion and metastasis. The  
CC invention provides methods for diagnosing, preventing, or treating a  
CC disease or disorder characterized by epithelial cell migration, increased  
CC tyrosine phosphorylation of beta-catenin, and/or increased levels of the  
CC pool of free beta-catenin, especially cancer, metastasis and aberrant  
CC wound healing (claimed). The methods may also be used to treat diseases  
CC and disorders with abnormal cell proliferative conditions, including  
CC fibrotic and mesangial disorders, abnormal angiogenesis and  
CC vasculogenesis, psoriasis, diabetes mellitus and inflammation. Methods  
CC are provided for identifying compounds that modulate PTP LAR activity for  
CC use in treatment

XX Sequence 1897 AA;

SQ Query Match 3.5%; Score 14; DB 3; Length 1897;

Best Local Similarity 100.0%; Pred. NO. 0.00016;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370

Db 1827 VHCSAGVGRGTGVFI 1840

RESULT 46

ADD18740

ID ADD18740 standard; protein; 1897 AA.

XX AC ADD18740;

XX 15-JAN-2004 (first entry)

DE Human disease related protein SeqID171.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;  
KW antiarteriosclerotic; vulnery; gene therapy;  
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;  
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;  
KW glucose transportation; catecholamine synthesis; iron transport;  
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;  
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;  
KW inflammatory condition; wound healing.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-03003892.

XX 23-AUG-2001; 2001GB-00020558.

PR 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

PI Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

DR N-PSDB; ADD18741.

XX New substantially purified polypeptide, useful for diagnosing or treating  
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion  
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or  
PT wound healing.

XX Claim 25; SEQ ID NO 171; 424pp; English.

XX This invention relates to novel human genes and gene product which are  
CC implicated in certain disease states. Compounds which modulate the  
CC proteins of the invention may have cytostatic, antiinflammatory, the  
CC ophthalmological, antiarteriosclerotic or vulnery activities. The  
CC sequences of the invention may be useful for gene therapy. The invention  
CC may be useful for diagnosing or treating a hypoxia-regulated condition,  
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,  
CC erythropoiesis, or the biological response to hypoxia conditions  
CC including processes such as glycolysis, gluconeogenesis, glucose  
CC transportation, catecholamine synthesis, iron transport or nitric oxide  
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion  
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,  
CC inflammatory conditions or wound healing. The present sequence is that of  
CC a disease related protein of the invention.

XX Sequence 1897 AA;

SQ Query Match 3.5%; Score 14; DB 7; Length 1897;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370

Db 1827 VHCSAGVGRGTGVFI 1840

RESULT 47

ABB57100

ID ABB57100 standard; protein; 1904 AA.

XX AC ABB57100;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:224.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX WO200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX 18-MAY-2000; 2000JP-00145977.

XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

DR WPI; 2002-034733/04.

DR N-PSDB; AB199344.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or by  
PT determining the expression profile of a gene group comprising these  
PT genes.

PS Claim 2; Page 636-644; 2690pp; English.

CC The present invention describes a method for examining ischaemic  
CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring the  
CC expression levels of particular genes (AB199202 to AB199912, encoding the  
CC protein sequences in AB57020 to AB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The expression  
CC levels or expression profiles produced by these genes are used as an  
CC indicator when screening for ischaemic condition-improving drugs or  
CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR  
CC primers for a mouse ischaemic condition related sequence, which are used  
CC in the exemplification of the present invention

XX Sequence 1904 AA;

Query Match 3.5%; Score 14; DB 5; Length 1904;  
Best Local Similarity 100.0%; Pred.No. 0.00016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370  
DB 1834 VHCAGVGTGVFI 1847  
|||||

RESULT 48

AAU14143  
ID AAU14143 standard; protein; 1907 AA.

AC AAU14143;

DT 24-OCT-2001 (first entry)

DE Human novel protein #14.

KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cyostatic; neuroprotective; vulnerary; nootropic;  
KW anticonvulsant; antithratic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.

XX Homo sapiens.

OS WO200155437-A2.

PN 02-AUG-2001.

PD 25-JAN-2001; 2001WO-US002623.

PF 25-JAN-2000; 2000US-00491404.

PR {HYSE-} HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

DR N-PSDB; AAS22448.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
XX nervous system disorders, and for regenerating bone and cartilage.

PS Example 4; Page 533-537; 894pp; English.

CC The invention relates to polynucleotides encoding novel human proteins or  
CC their active domains. The polypeptides, polynucleotides and antibodies  
CC raised against the polypeptides are used in a method of treatment of a  
CC mammal and prevention of disorders caused by the aberrant protein  
CC expression or activity. The polypeptides can be used as molecular weight

CC markers, food supplements, and in antibody production. The polypeptides  
CC are used to identify compounds which bind to the polypeptides.  
CC Polynucleotides of the invention are used as probes and primers, for  
CC sequencing, for chromosome or gene mapping, in the production of  
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene  
CC therapy. Polypeptides of the invention can be used to target drugs to a  
CC tumour, in assays to determine biological activity, to raise  
CC antibodies/felicit an immune response, to determine quantitative protein  
CC levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-  
CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory  
CC diseases, nervous system disorders, and infection. The present sequence  
CC represents a protein of the invention

XX Sequence 1907 AA;

Query Match 3.5%; Score 14; DB 4; Length 1907;  
Best Local Similarity 100.0%; Pred.No. 0.00016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVFI 370

DB 1837 VHCAGVGTGVFI 1850  
|||||

RESULT 49

AAR71726  
ID AAR71726 standard; protein; 1911 AA.

XX AAR71726;

DT 25-MAR-2003 (revised)

DT 17-OCT-1995 (first entry)

XX Human PTP-OB.

XX PTP-OB; protein tyrosine phosphatase; osteoblast; differentiation;  
XX osteoclast; osteoporosis; bone; cancer; osteosarcoma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..29

FT Modified-site /label= Sig\_peptide

FT Modified-site 250

FT Modified-site /label= N-glycosylation\_site

FT Modified-site 721

FT Modified-site /label= N-glycosylation\_site

FT Domain 919

FT Domain /label= N-glycosylation\_site

FT Domain 1253..1277

FT Domain /label= Extracellular\_domain

XX WO9507935-A1.

XX 23-MAR-1995.

XX 09-SEP-1994; 94WO-US010166.

XX 14-SEP-1993; 93US-00122032.

XX (MERI ) MERCK & CO INC.

XX Rodan GA, Rutledge SJ, Schmidt A;

XX WPI; 1995-131318/17.

DR N-PSDB; AAQ86478.  
 XX Protein tyrosine phosphatase protein PTP-OB specifically expressed in bone  
 PT cells - modulators of which are used to treat, e.g. osteoporosis, and  
 PT prevent and treat bone loss and cancer.  
 XX Claim 1; Page 44-45; 63pp; English.  
 XX PCR amplification of cDNA derived from human osteosarcoma Saos-2/B10  
 CC using primers based on conserved regions of protein tyrosine phosphatases  
 CC and subsequent screening of a human brain cDNA library yielded a cDNA  
 CC clone (sequence given in AAQ86473) that encoded a novel human protein,  
 CC PTP-OB (AAR71726). Recombinant PTP-OB was expressed in E. coli, yeast,  
 CC insect and mammalian cells. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 1911 AA;  
 SQ

Query Match 3.5%; Score 14; DB 2; Length 1911;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1841 VHCAGVGRGTGVFI 1854

RESULT 50  
 AAW27225  
 ID AAW27225 standard; protein; 1911 AA.  
 XX  
 AC AAW27225;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 19-DEC-1997 (first entry)  
 DT  
 XX Human protein tyrosine phosphatase PTP-OB.  
 XX Protein tyrosine phosphatase, PTP-OB; PTPepsilon; osteoblast;  
 KW recombinant protein; growth; differentiation; brain; human.  
 XX Homo sapiens.  
 OS  
 XX US5658756-A.  
 PN  
 XX 19-AUG-1997.  
 PD  
 XX 01-DEC-1994; 94US-00348006.  
 PF  
 XX 14-SEP-1993; 93US-00122032.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Schmidt A, Rodan GA, Rutledge SJ;  
 PI WPI; 1997-424232/39.  
 XX N-PSDB; AAT85389.  
 DR DNA encoding protein tyrosine phosphatase PTP-OB - isolated from human  
 PT osteoblasts and useful for production of recombinant PTP-OB.  
 XX  
 XX Claim 1; Col 23-34; 34pp; English.  
 PS The present sequence represents human protein tyrosine phosphatase (PTP-  
 CC OB) protein. The DNA encoding this protein is useful for the production  
 CC of the recombinant protein, which is a protein tyrosine phosphatase which  
 CC may be involved in the growth and differentiation of osteoblasts and  
 CC brain cells and is useful for identifying compounds that modulate PTP-OB  
 CC activity and as a therapeutic agent for treating PTP-OB-related diseases.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 1911 AA;  
 SQ

Query Match 3.5%; Score 14; DB 2; Length 1911;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1841 VHCAGVGRGTGVFI 1854

RESULT 51  
 AAW94027  
 ID AAW94027 standard; protein; 1911 AA.  
 XX  
 AC AAW94027;  
 XX  
 DT 01-APR-1999 (first entry)  
 DT  
 XX Human protein tyrosine phosphatase (PTP-OB).  
 XX Protein tyrosine phosphatase; PTP; PTP-OB; bone; brain; cancer;  
 KW osteoporosis.  
 XX Homo sapiens.  
 OS  
 XX US5866397-A.  
 PN  
 XX 02-FEB-1999.  
 PD  
 XX 14-FEB-1997; 97US-00800825.  
 PF  
 XX 14-SEP-1993; 93US-00122032.  
 PR  
 XX 01-DEC-1994; 94US-00348006.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Rutledge SJ, Schmidt A, Rodan GA;  
 PI WPI; 1999-141930/12.  
 XX N-PSDB; AAX06095.  
 DR Protein tyrosine phosphatase denoted PTP-OB - useful for drug screening.  
 XX  
 XX Claim 1; Col 23-32; 34pp; English.  
 PS This represents a human protein tyrosine phosphatase (PTP) denoted as PTP  
 CC -OB, produced by bone and brain cells. A recombinant host cell  
 CC transfected or transformed with a nucleic acid vector comprising the  
 CC nucleic acid can be used for the production of the PTP-OB polypeptide.  
 CC The protein can be used to screen for modulators of PTP-OB activity,  
 CC which might be useful for treating e.g. osteoporosis and cancer  
 XX Sequence 1911 AA;

Query Match 3.5%; Score 14; DB 2; Length 1911;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 DB 1841 VHCAGVGRGTGVFI 1854

RESULT 52  
 AAU01459  
 ID AAU01459 standard; protein; 1911 AA.  
 XX  
 AC AAU01459;  
 XX  
 DT 18-JUL-2001 (first entry)  
 DT  
 XX Human protein tyrosine phosphatase, PTP-OB, amino acid sequence.  
 XX Protein tyrosine phosphatase; PTP; human; osteoporosis; bone formation;  
 KW PTP-OB; cell proliferation; cell death; neoplastic transformation;

KW metastasis; tumour; cancer; lung cancer; osteosarcoma.  
 XX Homo sapiens.  
 XX US6214564-B1.  
 XX 10-APR-2001.  
 XX 22-SEP-1998; 98US-00158557.  
 XX 14-SEP-1993; 93US-00122032.  
 XX 01-DEC-1994; 94US-00348006.  
 XX 14-FEB-1997; 97US-00800825.  
 XX (MERI ) MERCK & CO INC.  
 XX Rodan GA, Rutledge SJ, Schmidt A;  
 XX WPI; 2001-280994/29.  
 XX N-PSDB; AAS02144.  
 XX Identifying a compound which modulates protein tyrosine phosphatase  
 PT activity for treating osteoporosis, comprises contacting a polypeptide  
 PT with a compound and measuring the ability of the compound to modulate  
 PT polypeptide activity.  
 XX Claim 1; Col 23-33; 35pp; English.  
 XX The sequence represents the amino acid sequence of human protein tyrosine  
 CC phosphatase, PTP-OB. The PTP-OB nucleic acid and protein sequences were  
 CC used in a method to identify a compound able to modulate PTP-OB activity,  
 CC involving contacting a recombinant polypeptide comprising the entire  
 CC cytoplasmic domain of PTP-OB with the compound, and measuring the ability  
 CC of the compound to modulate the activity of the polypeptide. The  
 CC compounds that modulate PTP-OB activity are useful in treating disease  
 CC states involving PTP-OB activity such as osteoporosis, for preventing and  
 CC treating bone loss, and stimulation of bone formation. The compounds are  
 CC also useful for treating diseases in which activation or inactivation of  
 CC PTP-OB protein results in either cellular proliferation, cell death,  
 CC nonproliferation, induction of cellular neoplastic transformations or  
 CC metastatic tumour growth, such as cancer, preferably lung cancer or  
 CC osteosarcoma  
 XX Sequence 1911 AA;  
 SQ Query Match 3.5%; Score 14; DB 4; Length 1911;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCASGVGRTGVFI 370  
 |||||  
 Db 1841 VHCASGVGRTGVFI 1854  
 RESULT 53  
 ADD18742  
 ID ADD18742 standard; protein; 1948 AA.  
 XX AC  
 XX ADD18742;  
 XX 15-JAN-2004 (first entry)  
 XX Human disease related protein SeqID173.  
 XX human; disease state; cytostatic; antiinflammatory; ophthalmological;  
 KW antiarteriosclerotic; vulnary; gene therapy;  
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;  
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;  
 KW glucose transportation; catecholamine synthesis; iron transport;  
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;  
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;  
 KW inflammatory condition; wound healing.

OS Homo sapiens.  
 XX WO2003018621-A2.  
 XX 06-MAR-2003.  
 XX 23-AUG-2002; 2002WO-GB003892.  
 XX 23-AUG-2001; 2001GB-00020558.  
 XX 05-OCT-2001; 2001GB-00024037.  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;  
 XX WPI; 2003-290046/28.  
 XX N-PSDB; ADD18743.  
 XX New substantially purified polypeptide, useful for diagnosing or treating  
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion  
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or  
 PT wound healing.  
 XX Claim 25; SEQ ID NO 173; 424pp; English.  
 XX This invention relates to novel human genes and gene product which are  
 CC implicated in certain disease states. Compounds which modulate the  
 CC proteins of the invention may have cytostatic, antiinflammatory,  
 CC ophthalmological, antiarteriosclerotic or vulnary activities. The  
 CC sequences of the invention may be useful for gene therapy. The invention  
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,  
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,  
 CC erythropoiesis, or the biological response to hypoxia conditions  
 CC including processes such as glycolysis, gluconeogenesis, glucose  
 CC transportation, catecholamine synthesis, iron transport or nitric oxide  
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion  
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,  
 CC inflammatory conditions or wound healing. The present sequence is that of  
 CC a disease related protein of the invention.  
 XX Sequence 1948 AA;  
 SQ Query Match 3.5%; Score 14; DB 7; Length 1948;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCASGVGRTGVFI 370  
 |||||  
 Db 1878 VHCASGVGRTGVFI 1891  
 RESULT 54  
 ADE57117  
 ID ADE57117 standard; protein; 1949 AA.  
 XX AC  
 XX ADE57117;  
 XX 29-JAN-2004 (first entry)  
 XX Human Protein U35234, SEQ ID NO 2977.  
 XX Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX Homo sapiens.  
 XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX





XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; U55234.

XX New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI), chronic constriction injury (CCI), and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1949 AA;

Query Match 3.5%; Score 14; DB 7; Length 1949;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370

DB 1878 VHCSAGVGRGTGVFI 1891

RESULT 57

ADD47015

ID ADD47015 standard; protein; 1949 AA.

XX ADD47015;

XX 29-JAN-2004 (first entry)

XX

DE Human Protein U55234, SEQ ID NO 12701.

XX

KN Human; pain; neuronal tissue; gene therapy;  
KN spinal segmental nerve injury; chronic constriction injury; CCI;  
KN spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

XX

PR 01-NOV-2001; 2001US-0346382P.

XX

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO ) GEN HOSPITAL CORP.

XX

PA (FARB ) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

XX WPI; 2003-268312/26.

XX

DR GENBANK; U55234.

XX

XX Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also

CC

CC

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CC

Query Match 3.5%; Score 14; DB 7; Length 1949;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370

DB 1878 VHCSAGVGRGTGVFI 1891

RESULT 58

AAE37322

ID AAE37322 standard; protein; 1959 AA.  
 XX AAE37322;  
 AC  
 DT 07-AUG-2003 (first entry)  
 XX  
 DE Human receptor tyrosine kinase protein #3.  
 XX  
 KW Human; receptor tyrosine phosphatase; diabetes; obesity; CNS disorder;  
 KW multiple sclerosis; epilepsy; chronic obstructive pulmonary disease;  
 KW COPD; Parkinson's disease; stroke; cardiovascular disorder; arrhythmia;  
 KW congestive heart failure; myocardial infarction; ischaemic heart disease;  
 KW gene therapy; anorectic; cardiac; neuroprotective; anticonvulsant;  
 KW cerebroprotective; vasotropic; antiarrhythmic; receptor; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003033688-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 14-OCT-2002; 2002WO-EP011473.  
 XX  
 PR 16-OCT-2001; 2001US-0329329P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Liou J;  
 XX  
 DR WPI; 2003-403215/38.  
 DR N-PSDB; AAD56413.  
 XX  
 XX Novel polynucleotides encoding human receptor tyrosine phosphatase  
 PT polypeptides, useful for treating diabetes, CNS disorders, obesity,  
 PT chronic obstructive pulmonary disease and cardiovascular disorders.  
 XX  
 PS Disclosure; Fig 5; 163pp; English.  
 XX  
 CC The present invention relates to receptor tyrosine phosphatase proteins  
 CC and polynucleotides encoding them. Sequences of the invention are useful  
 CC in the preparation of medicaments for modulating the activity of receptor  
 CC tyrosine phosphatase in disease such as diabetes, obesity, CNS disorders  
 CC (multiple sclerosis, epilepsy, Parkinson's disease and stroke), chronic  
 CC obstructive pulmonary disease (COPD) and cardiovascular disorders (e.g.  
 CC congestive heart failure, myocardial infarction, ischaemic heart disease  
 CC and arrhythmia). They are also used in gene therapy. The present sequence  
 CC is human receptor tyrosine kinase protein  
 XX  
 SQ Sequence 1959 AA;  
 Query Match 3.5%; Score 14; DB 6; Length 1959;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGTGVFI 370  
 DB 1858 VHCAGVGRGTGVFI 1871  
 RESULT 59  
 AAO18736  
 ID AAO18736 standard; protein; 2281 AA.  
 XX  
 AC AAO18736;  
 XX  
 DT 24-OCT-2002 (first entry)  
 XX  
 DE Human NOV2a protein.  
 XX  
 KW Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;  
 KW storage disorder; muscle disorder; neurodegenerative disorder; neurotropic;  
 KW developmental defect; neuroprotective; antiparkinsonian; hypotensive;  
 KW hypertensive; haemostatic; cardiac; antianginal; dermatological;

KW immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;  
 KW antiparasitic; antiallergic; antiasthmatic; antirheumatic; antiarthritic;  
 KW vulnery; anorectic; antidiabetic; immunomodulator; antipsoriatic;  
 KW nephrotropic; kerolytic; antitumor; cerebroprotective; anticonvulsant;  
 KW antinfertility; antitumor; antidepressant; metabolic; cytostatic;  
 KW tranquilizer; analgesic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257450-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 29-NOV-2001; 2001WO-US048922.  
 XX  
 PR 29-NOV-2000; 2000US-0253834P.  
 PR 30-NOV-2000; 2000US-0250926P.  
 PR 25-JAN-2001; 2001US-0264180P.  
 PR 20-AUG-2001; 2001US-0313656P.  
 PR 05-OCT-2001; 2001US-0327456P.  
 PR 28-NOV-2001; 2001US-00327456.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Edinger S, MacDougall JR, Millet I, Ellerman K, Stone DJ;  
 PI Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CE;  
 PI Casman SJ, Spytek KA, Boldog FL, Li L, Padigaru M, Mishra V;  
 PI Pattrajan M, Shenoy S, Rastelli L, Tchernev VT, Vermet CAM;  
 PI Zerhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;  
 XX  
 DR WPI; 2002-590741/63.  
 DR N-PSDB; ABT06281.  
 XX  
 XX Novel isolated polypeptide, designated NOVX, useful for treating or  
 PT preventing in NOVX-associated disorders e.g. cardiomyopathy,  
 PT atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.  
 XX  
 PS Claim 1; Page 25-26; 353pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of  
 CC several novel human proteins, designated NOVX. These can be used in the  
 CC treatment of, amongst others, cancers, autoimmune diseases, infections,  
 CC inflammatory diseases, storage disorders, muscle disorders,  
 CC neurodegenerative diseases and developmental defects. The present  
 CC sequence is a protein of the invention  
 XX  
 SQ Sequence 2281 AA;  
 Query Match 3.5%; Score 14; DB 5; Length 2281;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGRGTGVFI 370  
 DB 2179 VHCAGVGRGTGVFI 2192  
 RESULT 60  
 ABP60057  
 ID ABP60057 standard; protein; 2291 AA.  
 XX  
 AC ABP60057;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human phosphatase protein SEQ ID #2.  
 XX  
 KW Human; phosphatase; enzyme; chromosome 12; colon adenocarcinoma;  
 KW placenta; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279452-A2.

XX 10-OCT-2002.  
PD  
XX  
XX 02-APR-2002; 2002WO-US009992.  
XX  
XX 02-APR-2001; 2001US-00822871.  
PR  
XX (PEKE ) PE CORP NY.  
XX  
XX Webster M, Wei M, Di Francesco V, Beasley EM;  
PI  
XX WPI; 2003-046909/04.  
DR  
DR N-PSDB; ABZ23703.  
XX  
XX New human phosphatase peptides and nucleic acids encoding the peptides,  
PT useful as models in developing human therapeutic targets, in identifying  
PT therapeutic proteins or modulators of protein activity, and in gene  
PT therapy.  
XX  
XX Claim 1a; Fig 2; 220pp; English.  
PS  
XX The invention relates to an isolated human phosphatase peptide. The human  
CC phosphatase peptides and nucleic acids are useful as models for the  
CC development of human therapeutic targets and in the identification of  
CC therapeutic proteins. They also serve as targets for the development of  
CC human therapeutic agents that modulate phosphatase activity in cells and  
CC tissues that express the phosphatase. Experimental data indicates that  
CC the cDNA is expressed in colon adenocarcinoma and placenta. The proteins  
CC can be used to raise or to elicit another immune response, as a reagent  
CC in assays designed to determine the levels of the protein in biological  
CC fluids, as markers for tissue in which the corresponding protein is  
CC preferentially expressed, in the identification of modulators of the  
CC peptides, and in pharmacogenomic analysis. The polypeptides and  
CC polynucleotides may be used in in gene therapy, and as antisense  
CC constructs to control phosphatase gene expression in cells, tissue and  
CC organisms. The gene encoding the phosphatase of the invention is located  
CC on human chromosome 12. The current sequence represents the human  
XX phosphatase protein of the invention  
XX  
SQ Sequence 2291 AA;  
Query Match 3.5%; Score 14; DB 6; Length 2291;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 357 VHCAGVGTGVFI 370  
Db 2190 VHCAGVGTGVFI 2203  
|||||  
RESULT 61  
AAG79724  
ID AAG79724 standard; protein; 2299 AA.  
XX  
XX AAG79724;  
AC  
XX  
XX 04-MAR-2003 (first entry)  
DT  
XX  
XX Human KPP-2, Incyte ID No. 7480588CD1.  
DE  
XX Kinase; phosphatase; KPP; cell proliferation; arteriosclerosis;  
KW atherosclerosis; cirrhosis; hepatitis; reproduction; infertility;  
KW paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;  
KW primary thrombocytopenia; cancer; development; renal tubular acidosis;  
KW anaemia; mental retardation; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; epilepsy; Sjogren's syndrome; uveitis; asthma;  
KW menstrual cycle; autoimmune; inflammation; rheumatoid arthritis; AIDS;  
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; allergy;  
KW diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout;  
KW Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;  
KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;  
KW Reiter's syndrome; rat; glomerular mesangial cell receptor protein;  
KW tyrosine phosphatase precursor; enzyme.

XX OS Homo sapiens.  
XX  
XX Key  
FH Peptide  
FT /label= Signal peptide  
FT /note= "Identified using HMMER"  
FT 1. .17  
FT /label= Signal peptide  
FT /note= "Identified using HMMER"  
FT 17  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 28  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 51. .138  
FT Domain  
FT /label= Fibronectin\_type\_III\_domain  
FT /note= "Identified using HMMER\_PPFAM"  
FT 66. .91  
FT Protein  
FT /label= Receptor tyrosine kinase class\_V\_protein  
FT /note= "Identified using BLIMPS\_BLOCKS"  
FT 104  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 115. .145  
FT Protein  
FT /label= Receptor tyrosine kinase class\_V\_protein  
FT /note= "Identified using BLIMPS\_BLOCKS"  
FT 120  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 145. .205  
FT Domain  
FT /label= Glomerular\_mesangial\_cell\_receptor  
FT /note= "Identified using BLAST\_PRODOM"  
FT 150. .286  
FT Domain  
FT /label= Fibronectin\_type\_III\_domain  
FT /note= "Identified using HMMER\_PPFAM"  
FT 155  
FT Modified-site  
FT /note= "Potentially glycosylated"  
FT 162  
FT Modified-site  
FT /note= "Potentially glycosylated"  
FT 182  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 186  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 200  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 208  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 249  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 298  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 300. .383  
FT Domain  
FT /label= Fibronectin\_type\_III\_domain  
FT /note= "Identified using HMMER\_PPFAM"  
FT 311  
FT Modified-site  
FT /note= "Potentially glycosylated"  
FT 313  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 328  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 332  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 349  
FT Modified-site  
FT /note= "Potentially glycosylated"  
FT 350  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 365  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 384  
FT Modified-site  
FT /note= "Potentially glycosylated"  
FT 389  
FT Modified-site  
FT /note= "Potentially phosphorylated"  
FT 394. .554  
FT Domain  
FT /label= Fibronectin\_type\_III\_domain  
FT /note= "Identified using HMMER\_PPFAM"

FT Modified-site 413 /note= "Potentially phosphorylated"

FT Modified-site 490 /note= "Potentially phosphorylated"

FT Modified-site 511 /note= "Potentially phosphorylated"

FT Modified-site 557 /note= "Potentially phosphorylated"

FT Domain 565..651

FT /label= Fibronectin\_type\_III\_domain

FT /note= "Identified using HMW\_PPFAM"

FT Modified-site 567 /note= "Potentially phosphorylated"

FT Modified-site 575 /note= "Potentially glycosylated"

FT Modified-site 607 /note= "Potentially phosphorylated"

FT Modified-site 614 /note= "Potentially phosphorylated"

FT Modified-site 623 /note= "Potentially phosphorylated"

FT Modified-site 633 /note= "Potentially phosphorylated"

FT Modified-site 649 /note= "Potentially phosphorylated"

FT Modified-site 660 /note= "Potentially phosphorylated"

FT Modified-site 661 /note= "Potentially phosphorylated"

FT Domain 665..746

FT /label= Fibronectin\_type\_III\_domain

FT /note= "Identified using HMW\_PPFAM"

FT Modified-site 668 /note= "Potentially phosphorylated"

FT Modified-site 678 /note= "Potentially phosphorylated"

FT Modified-site 687 /note= "Potentially phosphorylated"

FT Modified-site 710 /note= "Potentially phosphorylated"

FT Modified-site 713 /note= "Potentially phosphorylated"

FT Modified-site 715 /note= "Potentially glycosylated"

FT Modified-site 731 /note= "Potentially phosphorylated"

FT Modified-site 733 /note= "Potentially glycosylated"

FT Modified-site 751 /note= "Potentially phosphorylated"

FT Modified-site 757 /note= "Potentially phosphorylated"

FT Domain 759..842

FT /label= Fibronectin\_type\_III\_domain

FT /note= "Identified using HMW\_PPFAM"

FT Modified-site 761 /note= "Potentially phosphorylated"

FT Modified-site 765 /note= "Potentially glycosylated"

FT Modified-site 767 /note= "Potentially phosphorylated"

FT Modified-site 770 /note= "Potentially glycosylated"

FT Modified-site 772 /note= "Potentially phosphorylated"

FT Modified-site 809 /note= "Potentially glycosylated"

FT Modified-site 824 /note= "Potentially phosphorylated"

FT Modified-site 834 /note= "Potentially phosphorylated"

FT Modified-site 849 /note= "Potentially phosphorylated"

FT Domain 854..936

FT /label= Fibronectin\_type\_III\_domain

FT /note= "Identified using HMW\_PPFAM"

FT Modified-site 862 /note= "Potentially phosphorylated"

FT Modified-site 870 /note= "Potentially phosphorylated"

FT Modified-site 895 /note= "Potentially glycosylated"

FT Modified-site 898 /note= "Potentially phosphorylated"

FT Modified-site 903 /note= "Potentially glycosylated"

FT Modified-site 907 /note= "Potentially phosphorylated"

FT Modified-site 912 /note= "Potentially phosphorylated"

FT Modified-site 927 /note= "Potentially phosphorylated"

FT Domain 948..1040

FT /label= Fibronectin\_type\_III\_domain

FT /note= "Identified using HMW\_PPFAM"

FT Modified-site 959 /note= "Potentially glycosylated"

FT Modified-site 988 /note= "Potentially glycosylated"

FT Modified-site 996 /note= "Potentially glycosylated"

FT Modified-site 998 /note= "Potentially phosphorylated"

FT Modified-site 1008 /note= "Potentially glycosylated"

FT Modified-site 1013

Query Match 3.5%; Score 14; DB 6; Length 2299;

Best Local Similarity 100.0%; Pred.No. 0.00019;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRTGVFI 370  
|||||

Db 2198 VHCAGVGRTGVFI 2211

RESULT 62

AAE37320

ID AAE37320 standard; protein; 2299 AA.

XX

AC AAE37320;

XX

XX 07-AUG-2003 (first entry)

XX Human receptor tyrosine kinase protein #1.

XX Human; receptor tyrosine phosphatase; diabetes; obesity; CMS disorder;

XX multiple sclerosis; epilepsy; chronic obstructive pulmonary disease;

XX COPD; Parkinson's disease; stroke; cardiovascular disorder; arrhythmia;

XX congestive heart failure; myocardial infarction; ischaemic heart disease;

XX gene therapy; anorectic; cardiant; neuroprotective; anticonvulsant;

XX cerebroprotective; vasotropic; antiarrhythmic; receptor; enzyme;

XX chromosome 12.

XX Homo sapiens.

OS

XX WO2003033688-A1.

PN

XX 24-APR-2003.

PD

XX 14-OCT-2002; 2002WO-EP011473.

PF

XX 16-OCT-2001; 2001US-0329329P.

PR

XX (FARB ) BAYER AG.

PA

XX

PI Liou J;  
 XX WPI; 2003-403215/38.  
 DR N-PSDB; AAD56411.  
 XX  
 XX Novel polynucleotides encoding human receptor tyrosine phosphatase  
 PT polypeptides, useful for treating diabetes, CNS disorders, obesity,  
 PT chronic obstructive pulmonary disease and cardiovascular disorders.  
 XX  
 XX Claim 1; Fig 2; 163pp; English.  
 XX  
 CC The present invention relates to receptor tyrosine phosphatase proteins  
 CC and polynucleotides encoding them. Sequences of the invention are useful  
 CC in the preparation of medicaments for modulating the activity of receptor  
 CC tyrosine phosphatase in disease such as diabetes, obesity, CNS disorders  
 CC (multiple sclerosis, epilepsy, Parkinson's disease and stroke), chronic  
 CC obstructive pulmonary disease (COPD) and cardiovascular disorders (e.g.  
 CC congestive heart failure, myocardial infarction, ischaemic heart disease  
 CC and arrhythmia). They are also used in gene therapy. The present sequence  
 CC is human receptor tyrosine kinase protein. Receptor tyrosine kinase gene  
 CC is located on chromosome 12  
 XX  
 SQ Sequence 2299 AA;  
 Query Match 3.5%; Score 14; DB 6; Length 2299;  
 Best Local Similarity 100.0%; Pred. No. 0.00019;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGTGVTGVP 370  
 DB 2198 VHCAGVGTGVTGVP 2211  
 RESULT 63  
 ID AA018738 standard; protein; 2300 AA.  
 AC AA018738;  
 DT 24-OCT-2002 (first entry)  
 DE Human NOV2c protein.  
 XX Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;  
 KW storage disorder; muscle disorder; neurodegenerative disorder; neurotic;  
 KW developmental defect; neuroprotective; antiparkinsonian; hypotensive;  
 KW hypertensive; haemostatic; cardiant; antianal; dermatological;  
 KW immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;  
 KW antiparasitic; antiallergic; antidiabetic; antirheumatic; antiarthritic;  
 KW vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic;  
 KW nephrotropic; kerolytic; antitumor; cerebroprotective; anticonvulsant;  
 KW antileptile; antitumor; antidiabetic; antipsoriatic; anticonvulsant;  
 KW tranquilizer; analgesic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257450-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 29-NOV-2001; 2001WO-US049522.  
 XX  
 PR 29-NOV-2000; 2000US-0253834P.  
 XX  
 PR 30-NOV-2000; 2000US-0250926P.  
 XX  
 PR 25-JAN-2001; 2001US-0264180P.  
 XX  
 PR 20-AUG-2001; 2001US-0313656P.  
 XX  
 PR 05-OCT-2001; 2001US-0327456P.  
 XX  
 PR 28-NOV-2001; 2001US-00327456.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Edinger S, MacDougall JR, Millet I, Ellerman K, Stone DJ;  
 PI Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CE;  
 PI

Casman SJ, Spytek KA, Boldog FL, Li L, Padigaru M, Mishra V;  
 Pi Pattarajan M, Shenoy S, Fastelli L, Tchernev VT, Vernet CAM;  
 Pi Zernhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;  
 XX  
 XX WPI; 2002-590741/63.  
 DR N-PSDB; ABT06283.  
 XX  
 XX Novel isolated polypeptide, designated NOVX, useful for treating or  
 PT preventing in NOVX-associated disorders e.g. cardiomyopathy,  
 PT atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.  
 XX  
 XX Claim 1; Page 30; 353pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of  
 CC several novel human proteins, designated NOVX. These can be used in the  
 CC treatment of, amongst others, cancers, autoimmune diseases, infections,  
 CC inflammatory diseases, storage disorders, muscle disorders,  
 CC neurodegenerative diseases and developmental defects. The present  
 CC sequence is a protein of the invention  
 XX  
 SQ Sequence 2300 AA;  
 Query Match 3.5%; Score 14; DB 5; Length 2300;  
 Best Local Similarity 100.0%; Pred. No. 0.00019;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 VHCAGVGTGVTGVP 370  
 DB 2199 VHCAGVGTGVTGVP 2212  
 RESULT 64  
 ID ABP60058 standard; protein; 2301 AA.  
 AC ABP60058;  
 XX  
 DT 21-MAR-2003 (first entry)  
 DE Human phosphatase related protein #SEQ ID 4.  
 XX Human; phosphatase; enzyme; chromosome 12; colon adenocarcinoma;  
 KW placenta; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279452-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 02-APR-2002; 2002WO-US009992.  
 XX  
 PR 02-APR-2001; 2001US-00822871.  
 XX  
 XX (PEKE ) PE CORP NY.  
 XX  
 XX Webster M, Wei M, Di Francesco V, Beasley EM;  
 PI WPI; 2003-046809/04.  
 DR  
 XX  
 XX New human phosphatase peptides and nucleic acids encoding the peptides,  
 PT useful as models in developing human therapeutic targets, in identifying  
 PT therapeutic proteins or modulators of protein activity, and in gene  
 XX therapy.  
 XX  
 PS Disclosure; Page 216-220; 220pp; English.  
 XX  
 CC The invention relates to an isolated human phosphatase peptide. The human  
 CC phosphatase peptides and nucleic acids are useful as models for the  
 CC development of human therapeutic targets and in the identification of  
 CC therapeutic proteins. They also serve as targets for the development of  
 CC human therapeutic agents that modulate phosphatase activity in cells and  
 CC tissues that express the phosphatase. Experimental data indicates that

CC the cDNA is expressed in colon adenocarcinoma and placenta. The proteins  
 CC can be used to raise or to elicit another immune response, as a reagent  
 CC in assays designed to determine the levels of the protein in biological  
 CC fluids, as markers for tissue in which the corresponding protein is  
 CC preferentially expressed, in the identification of modulators of the  
 CC peptides, and in pharmacogenomic analysis. The polypeptides and  
 CC polynucleotides may be used in gene therapy, and as antisense  
 CC constructs to control phosphatase gene expression in cells, tissue and  
 CC organisms. The gene encoding the phosphatase of the invention is located  
 CC on human chromosome 12. The current sequence represents a human  
 CC phosphatase protein related to the one of the invention  
 XX  
 SQ Sequence 2301 AA;

Query Match 3.5%; Score 14; DB 6; Length 2301;  
 Best Local Similarity 100.0%; Pred. No. 0.00019;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGVFI 370  
 DB 2200 VHCAGVGRGVFI 2213  
 |||||

RESULT 65  
 ABB56552  
 ID ABB56552 standard; peptide; 14 AA.

AC ABB56552;  
 DT 05-MAR-2002 (first entry)

DE Human SNP related amino acid sequence SEQ ID NO:1117.

KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
 KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
 KW autoimmune disease; inflammation; cancer; nervous system disease;  
 KW infection; polymorphic protein.

OS Homo sapiens.

PN W0200138586-A2.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000NO-US032311.

PR 24-NOV-1999; 99US-0167383P.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

XX WPI; 2001-355949/37.

XX Isolated human nucleic acids comprising one or more single nucleotide  
 CC polymorphisms, useful for treating a subject suffering from a pathology,  
 CC e.g. autoimmune diseases, ascribed to the presence of a sequence  
 CC polymorphism.

PS Claim 1; Page 588; 674pp; English.

XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 CC to ABB56903 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have  
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
 CC and antibodies from the present invention can be used for treating a  
 CC subject suffering from, at risk for, or suspected of, suffering from a  
 CC pathology ascribed to the presence of a sequence polymorphism. The  
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
 CC are also useful for determining which forms of a characterised

CC polymorphism are present in individuals. The antibodies may be used in  
 CC the detection, quantitation and/or cellular or tissue localisation of a  
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic  
 CC protein within appropriate physiological samples)

XX Sequence 14 AA;

Query Match 3.0%; Score 12; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 BEYFYIATQGPL 238  
 DB 2 BEYFYIATQGPL 13  
 |||||

RESULT 66  
 AAR20747  
 ID AAR20747 standard; protein; 245 AA.

AC AAR20747;

DT 25-MAR-2003 (revised)

DT 28-MAY-1992 (first entry)

DE Human R-PTase gamma first conserved phosphatase.

XX Receptor-type protein tyrosine phosphatase; cellular metabolism; cancer;  
 KW diabetes.

OS Homo sapiens.

PN W0201050-A.

PD 23-JAN-1992.

PF 11-JUL-1990; 90US-00551270.

PR 11-JUL-1990; 90US-00551270.

PR 26-FEB-1991; 91US-00654188.

XX (UNY ) UNIV NEW YORK STATE.

XX Schlessing J;

XX WPI; 1992-056865/07.

XX Human receptor-type protein tyrosine phosphatase - has DNA encoding it  
 CC and antibodies specific for it, useful for screening drugs affecting R-  
 CC ptase activity, and detect mutant genes.

PS Claim 5; Fig 5A; 77pp; English.

XX The amino acid sequence is that of human receptor-type protein tyrosine  
 CC phosphatase (R-PTase) gamma first conserved phosphatase. It is useful in  
 CC methods for screening drugs and other agents which are capable of  
 CC activating or inhibiting the R-PTase activity and thereby affecting  
 CC major pathways of cellular metabolism. Activation of R-PTases, leading  
 CC to dephosphorylation would serve as a counter-regulatory mechanism to  
 CC prevent or inhibit growth, and may serve as an endogenous regulatory  
 CC mechanism against cancer. Mutation or dysregulation of this  
 CC receptor/enzyme system may promote susceptibility to cancer, diabetes, or  
 CC other diseases associated with alterations in cellular phosphotyrosine  
 CC metabolism. It can be used to raise antibodies which can be used in  
 CC immunoassays to determine the presence and amt. of R-PTases, or in  
 CC immunoelectron microscopy for in situ detection of R-PTase. See also  
 CC AAR20743-R20748. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 245 AA;

Query Match 3.0%; Score 12; DB 2; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRG 367  
 DB 183 LVHCSAGVGRG 194

RESULT 67  
 AAB59381  
 ID AAB59381 standard; protein; 257 AA.

AC AAB59381;  
 XX 21-MAR-2001 (first entry)

XX Drosophila protein tyrosine phosphatase #3.

XX Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;

XX substrate trapping.

XX Drosophila sp.

XX WO200075339-A1.

XX 14-DEC-2000.

XX 24-MAY-2000; 2000WO-US014211.

XX 03-JUN-1999; 99US-0137319P.

XX 16-JUN-1999; 99US-00334575.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Tonks NK, Zhang S;

XX WPI; 2001-080598/09.

XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
 PT which the wild type PTP catalytic domain invariant aspartate is replaced  
 PT with an unphosphorylated amino acid, useful in gene therapy.

XX Disclosure; Fig 1; 109pp; English.

XX The present invention provides substrate trapping mutant protein tyrosine  
 CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
 CC phosphorylated proteins and to screen for modulators capable of altering  
 CC the binding of protein tyrosine phosphatases to their substrate. These  
 CC may be used in disease diagnosis and treatment

XX Sequence 257 AA;

Query Match 3.0%; Score 12; DB 4; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRG 367  
 DB 187 LVHCSAGVGRG 198

RESULT 68  
 AAG78279  
 ID AAG78279 standard; protein; 263 AA.

XX AAG78279;

XX 19-DEC-2001 (first entry)

XX Drosophila PTP69A-D1.

XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;  
 KW dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;  
 KW yeast.

OS Drosophila sp.  
 XX WO200161031-A2.  
 XX 23-ADG-2001.

XX 13-FEB-2001; 2001WO-US005180.

XX 14-FEB-2000; 2000US-0181769P.

XX (CEPT-) CEPTYR INC.

XX Flint AJ, Cool DE;

XX WPI; 2001-570570/64.

XX Screening assays to identify agents that alter protein tyrosine  
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic  
 PT dephosphorylation of phosphotyrosine peptide substrates.

XX Disclosure; Fig 1; 79pp; English.

XX The invention relates to identifying agents which alter the interaction  
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine  
 CC phosphorylated polypeptide using fluorescence energy signals. The methods  
 CC are useful for performing screening assay to identify agents that alter  
 CC PTP binding to and PTP-mediated catalytic dephosphorylation of  
 CC phosphotyrosine peptide substrates. The present sequence is that of a  
 CC catalytic domain of a PTP for comparison with human PTP1B (AAG78262)

XX Sequence 263 AA;

Query Match 3.0%; Score 12; DB 4; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRG 367  
 DB 187 LVHCSAGVGRG 198

RESULT 69

AAB59368  
 ID AAB59368 standard; protein; 263 AA.

XX AAB59368;

XX 21-MAR-2001 (first entry)

XX Human protein tyrosine phosphatase #5.

XX Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
 KW substrate trapping.

XX Homo sapiens.

XX WO200075339-A1.

XX 14-DEC-2000.

XX 24-MAY-2000; 2000WO-US014211.

XX 03-JUN-1999; 99US-0137319P.

XX 16-JUN-1999; 99US-00334575.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Tonks NK, Zhang S;

XX WPI; 2001-080598/09.

XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
 PT which the wild type PTP catalytic domain invariant aspartate is replaced



PT with an unphosphorylated amino acid, useful in gene therapy.

XX Disclosure; Fig 1; 109pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine  
phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
phosphorylated proteins and to screen for modulators capable of altering  
the binding of protein tyrosine phosphatases to their substrate. These  
may be used in disease diagnosis and treatment

XX Sequence 263 AA;

Query Match 3.0%; Score 12; DB 4; Length 283;

Best Local Similarity 100.0%; Pred.No. 0.0026;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367

DB 193 LVHCSAGVGRGTG 204

RESULT 70

AAAG78266  
ID AAG78266 standard; protein; 319 AA.

XX AC AAG78266;

XX DT 19-DEC-2001 (first entry)

XX DE Human PTP-gamma-D1.

XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;  
dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;  
yeast.

XX OS Homo sapiens.

XX FN WO200151031-A2.

XX PD 23-AUG-2001.

XX PF 13-FEB-2001; 2001WO-US005180.

XX PR 14-FEB-2000; 2000US-0181769P.

XX PA (CEPT-) CEPTYR INC.

XX PI Flint AJ, Cool DE;

XX DR WPI; 2001-570570/64.

XX Screening assays to identify agents that alter protein tyrosine  
phosphatase (PTP) binding to, and PTP-mediated catalytic  
dephosphorylation of phosphotyrosine peptide substrates.

XX Disclosure; Fig 1; 79pp; English.

XX The invention relates to identifying agents which alter the interaction  
between a protein tyrosine phosphatase (PTP) and a tyrosine  
phosphorylated polypeptide using fluorescence energy signals. The methods  
are useful for performing screening assay to identify agents that alter  
PTP binding to and PTP-mediated catalytic dephosphorylation of  
phosphotyrosine peptide substrates. The present sequence is that of a  
catalytic domain of a PTP for comparison with human PTP1B (AAG78262)

XX Sequence 319 AA;

Query Match 3.0%; Score 12; DB 4; Length 319;

Best Local Similarity 100.0%; Pred.No. 0.0032;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367

DB 193 LVHCSAGVGRGTG 204

DB 193 LVHCSAGVGRGTG 204

RESULT 71

AAAR85203

ID AAR85203 standard; protein; 1337 AA.

XX AC AAR85203;

XX DT 12-FEB-1996 (first entry)

XX DE huDEP-1.

XX Density enhanced Type III receptor-like protein tyrosine phosphatase;  
huDEP-1.

XX OS Homo sapiens.

XX FN WO9530008-A1.

XX PD 09-NOV-1995.

XX PF 03-MAY-1995; 95WO-US005512.

XX PR 03-MAY-1994; 94US-00237940.

XX PA (COLD-) COLD SPRING HARBOR LAB.

XX PI Tonks NK, Oestman A;

XX DR WPI; 1995-393079/50.

XX DR N-PSDB; AAT06027.

XX New density enhanced protein tyrosine phosphatase - used to develop  
prods. to modify transcription, translation and activity of tyrosine  
phosphatase(s).

XX Claim 4; Page 34-38; 51pp; English.

XX A cDNA clone was obtd. (see AAT06027) from a HeLa cell cDNA library that  
encoded a novel density-enhanced Type III receptor-like PTP, designated  
huDEP-1 (AAR85203). huDEP-1 is useful for the study of PTPs and for the  
development of therapeutic or prophylactic cpds. e.g. for prevention of  
abnormal or malignant cell growth

XX SQ Sequence 1337 AA;

Query Match 3.0%; Score 12; DB 2; Length 1337;

Best Local Similarity 100.0%; Pred.No. 0.012;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367

DB 1236 LVHCSAGVGRGTG 1247

RESULT 72

ABB65364

ID ABB65364 standard; protein; 1428 AA.

XX AC ABB65364;

XX DT 26-MAR-2002 (first entry)

XX OS Drosophila melanogaster polypeptide SEQ ID NO 22884.

XX Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical.

XX OS Drosophila melanogaster.

XX FN WO200171042-A2.

PD 27-SEP-2001.  
 XX 23-MAR-2001; 2001WO-US009231.  
 XX 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX (PEKE ) PE CORP NY.  
 PA Venter JC, Adams M, Li PMD, Myers EW;  
 PI WPI; 2001-656860/75.  
 XX N-PSDB; ABL09467.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 FT genes from Drosophila and for elucidating cell signaling and cell-cell  
 FT interactions.  
 FT  
 XX Disclosure; SEQ ID NO 22884; 21pp + Sequence Listing; English.  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 1428 AA;  
 SQ

Query Match 3.0%; Score 12; DB 4; Length 1428;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
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 DB 1060 LVHCSAGVGRGTG 1071

RESULT 73  
 AAR5809  
 ID AAR58809 standard; protein; 1445 AA.  
 XX  
 AC AAR58809;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-MAR-1995 (first entry)  
 XX  
 DE Human RPTP-gamma.  
 XX  
 XX RPTP-gamma; receptor tyrosine phosphatase-gamma; phosphatase; mapping;  
 KW gene therapy; tumor suppressor gene; kidney carcinoma; lung carcinoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT  
 FT Cleavage-site 53  
 FT /notes= "putative proteolytic cleavage site"  
 FT Domain 56..322  
 FT /label= Carbonic-anhydrase\_domain  
 FT Modified-site 109  
 FT /label= N-glycosylation\_site  
 FT Modified-site 113  
 FT /label= N-glycosylation\_site  
 FT Modified-site 156  
 FT /label= N-glycosylation\_site  
 FT Modified-site 359  
 FT /label= N-glycosylation\_site

FT Modified-site 444  
 FT /label= N-glycosylation\_site  
 FT Modified-site 619  
 FT /label= N-glycosylation\_site  
 FT Modified-site 631  
 FT /label= N-glycosylation\_site  
 FT Modified-site 722  
 FT /label= N-glycosylation\_site  
 FT Peptide 737..762  
 FT /label= Trans-membrane\_peptide  
 FT Domain 873..1118  
 FT /label= Phosphatase\_domain-DI  
 FT Domain 1175..1409  
 FT /label= Phosphatase\_domain-DII  
 XX  
 PN W09418309-A1.  
 XX  
 XX 18-AUG-1994.  
 XX  
 XX 09-FEB-1994; 94WO-US001542.  
 XX  
 XX 10-FEB-1993; 93US-00015986.  
 XX  
 XX (UNY ) UNIV NEW YORK STATE.  
 XX  
 XX Schlessinger J;  
 XX WPI; 1994-279730/34.  
 DR N-PSDB; AAQ71842.  
 XX  
 XX Human receptor-type tyrosine phosphatase-gamma (glyco)protein - used to  
 FT screen cpds that activate or inhibit protein phosphatases, and in gene  
 FT therapy.  
 XX  
 XX Disclosure; Fig 3A-3K; 93pp; English.  
 XX  
 XX cDNA encoding RPTP-gamma was isolated from a phage lambda-gt11 cDNA  
 CC library of 1-day-old human brain stem. The gene mapped to 3p14.2- p21, a  
 CC region deleted in certain types of renal and lung carcinomas, suggesting  
 CC its function as a tumor suppressor gene. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 XX Sequence 1445 AA;  
 SQ

Query Match 3.0%; Score 12; DB 2; Length 1445;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 |||||  
 DB 1057 LVHCSAGVGRGTG 1068

RESULT 74  
 ABR52348  
 ID ABR52348 standard; protein; 1705 AA.  
 XX  
 AC ABR52348;  
 XX  
 XX 19-JUN-2003 (first entry)  
 XX  
 XX Protein relating to the invention SEQ ID NO: 37.  
 XX  
 XX antiproliferative; hepatotropic; nephrotropic; antiarthritic;  
 KW antipsoriatic; cardiant; cycostatic; gene therapy; liver disease;  
 KW proliferative disorder; renal failure; cardiovascular disorder;  
 KW immunological disorder; arthritis; psoriasis; congenital heart defect;  
 KW congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.  
 XX  
 XX Mus musculus.  
 XX  
 PN W0200257460-A2.  
 XX

PD 25-JUL-2002.  
 XX 20-DEC-2001; 2001WO-US050459.  
 XX 20-DEC-2000; 2000US-0256868P.  
 XX 30-MAR-2001; 2001US-0280186P.  
 PR 01-MAY-2001; 2001US-0287733P.  
 PR 05-JUN-2001; 2001US-0295848P.  
 PR 25-JUN-2001; 2001US-0300465P.  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;  
 PI Siemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;  
 PI Krystek S, Meatee P, Suchard S, Banas D;  
 XX WPI; 2002-599721/64.  
 XX Novel polynucleotides encoding human phosphatase polypeptides useful in  
 PT the prevention or treatment of e.g. proliferative and cardiovascular  
 PT disorders.  
 XX Disclosure; Fig 9; 801pp; English.  
 XX The invention relates to a novel isolated nucleic acid comprising a  
 CC polynucleotide having a nucleotide sequence selected from 40  
 CC polynucleotides fully defined in the specification. The polynucleotide of  
 CC the invention has antiproliferative, hepatotropic, nephrotropic,  
 CC antiarthritic, antipeptidic, cardiant, and cytostatic activity. The  
 CC polynucleotide may have a use in gene therapy. A polynucleotide or  
 CC polypeptide of the invention is useful for preventing, treating or  
 CC ameliorating a medical condition, e.g. a proliferative disorder. They are  
 CC also useful for treating e.g. liver disease, renal failure, immunological  
 CC disorders including arthritis and psoriasis, cardiovascular disorders  
 CC such as congenital heart defects and congestive heart failure, and  
 CC cancer. A method of the invention is useful for diagnosing a pathological  
 CC condition or susceptibility to a condition in a subject. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 1705 AA;  
 Query Match 3.0%; Score 12; DB 5; Length 1705;  
 Best Local Similarity 100.0%; Pred.No. 0.015;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 LVHCSAGVGRGTG 367  
 DB 1347 LVHCSAGVGRGTG 1358  
 RESULT 75  
 AAW70506  
 ID AAW70506 standard; protein; 1711 AA.  
 AC AAW70506;  
 XX 29-DEC-1998 (first entry)  
 DE Osteostecticular protein tyrosine phosphatase protein.  
 DE Osteostecticular protein tyrosine phosphatase; OST-PTP; bone; testis;  
 KW osteoblast specific form; OST; OST-PTP receptor; osteoporosis;  
 KW osteopetrosis; bone metabolic disorder.  
 XX Rattus sp.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..17  
 FT /note= "Signal peptide"  
 FT 18..1711  
 FT /note= "OST-PTP"  
 FT 32..124  
 FT /note= "Fibronectin type III-like domain I"

FT Modified-site 117..119  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 125..215  
 FT /note= "Fibronectin type III-like domain II"  
 FT Domain 216..303  
 FT /note= "Fibronectin type III-like domain III"  
 FT Modified-site 239..241  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 259..261  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 304..392  
 FT /note= "Fibronectin type III-like domain IV"  
 FT Domain 393..470  
 FT /note= "Fibronectin type III-like domain V"  
 FT Modified-site 431..433  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 471..562  
 FT /note= "Fibronectin type III-like domain VI"  
 FT Modified-site 551..553  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 563..652  
 FT /note= "Fibronectin type III-like domain VII"  
 FT Modified-site 570..572  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 620..622  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 649..651  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 653..741  
 FT /note= "Fibronectin type III-like domain VIII"  
 FT Modified-site 663..665  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 737..739  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 742..830  
 FT /note= "Fibronectin type III-like domain IX"  
 FT Domain 831..921  
 FT /note= "Fibronectin type III-like domain X"  
 FT Modified-site 851..853  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 882..884  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 970..972  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 982..984  
 FT /note= "Asn is N-glycosylated"  
 FT Domain 1082..1104  
 FT /note= "Transmembrane domain"  
 FT Modified-site 1266..1268  
 FT /note= "Asn is N-glycosylated"  
 FT Active-site 1348..1359  
 FT /note= "Catalytic residues"  
 FT Modified-site 1569..1571  
 FT /note= "Asn is N-glycosylated"  
 FT Active-site 1668..1678  
 FT /note= "Catalytic residues"  
 XX US821084-A.  
 XX 13-OCT-1998.  
 XX 21-NOV-1994; 94US-00342930.  
 XX 21-NOV-1994; 94US-00342930.  
 XX (UNMI ) UNIV MICHIGAN.  
 XX (AMGP ) AMERICAN HOME PROD CORP.  
 XX Dixon JE, Olmsted EA, Mauro LJ, Davis AR;  
 XX WPI; 1998-567659/48.  
 XX N-PSDB; AAV33577.  
 XX

PT DNA encoding osteoblast-testicular protein tyrosine kinase polypeptide -  
PT useful for producing recombinant polypeptide.

XX  
PS Claim 4; Col 33-42; 31pp; English.  
XX  
CC The present sequence represents a rat osteotesticular protein tyrosine  
CC phosphatase (OST-PTP). OST-PTP is a transmembrane protein expressed only  
CC in bone and testis. The OST-PTP cDNA is useful for producing recombinant  
CC protein. The invention also provides a truncated osteoblast specific form  
CC (OST) containing the OST-PTP receptor but lacking the catalytic domain.  
CC The OST-PTP protein is claimed to be useful in assays used for screening  
CC abnormal bone growth patterns and metabolic bone diseases. The OST-PTP  
CC protein is also claimed to be useful in the treatment of osteoporosis,  
CC osteopetrosis and other bone metabolic disorders

XX SQ Sequence 1711 AA;  
Query Match 3.0%; Score 12; DB 2; Length 1711;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 356 LVHCSAGVGRGTG 367  
Db 1347 LVHCSAGVGRGTG 1358  
|||||

Search completed: June 21, 2004, 17:20:11  
Job time : 63 secs

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Title: US-09-095-478A-7

Perfect score: 405

Sequence: 1 MSSPRKVRGKTGRDNEEG.....DIMNIVTQMKQRCGMQIK 405

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	360	88.9	379	10	US-09-095-478-8
5	335	82.7	354	10	US-09-095-478-6
6	122	30.1	122	10	US-09-095-478-4
7	30	7.4	30	10	US-09-095-478-22
8	29	7.2	29	10	US-09-095-478-23
9	29	7.2	29	10	US-09-095-478-24
10	29	7.2	29	10	US-09-095-478-25
11	23	5.7	122	10	US-09-095-478-5
12	19	4.7	420	16	US-10-311-764-4
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15	14	3.5	176	14	US-10-314-232-9

## SUMMARIES

16	14	3.5	289	14	US-10-314-232-47	Sequence 47, Appl
17	14	3.5	294	9	US-09-788-626-27	Sequence 27, Appl
18	14	3.5	322	14	US-10-314-232-11	Sequence 11, Appl
19	14	3.5	344	16	US-10-408-765A-1670	Sequence 1670, Ap
20	14	3.5	401	14	US-10-314-232-15	Sequence 15, Appl
21	14	3.5	442	9	US-09-925-300-950	Sequence 950, App
22	14	3.5	647	15	US-10-291-365-722	Sequence 722, App
23	14	3.5	898	14	US-10-314-232-22	Sequence 22, Appl
24	14	3.5	1495	15	US-10-258-666-12	Sequence 12, Appl
25	14	3.5	1502	9	US-09-808-602-54	Sequence 54, Appl
26	14	3.5	1502	10	US-09-800-198-44	Sequence 44, Appl
27	14	3.5	1907	15	US-10-291-365-250	Sequence 250, App
28	14	3.5	1948	9	US-09-808-602-55	Sequence 55, Appl
29	14	3.5	1948	10	US-09-800-198-45	Sequence 45, Appl
30	14	3.5	2281	12	US-10-087-684-6	Sequence 6, Appli
31	14	3.5	2281	12	US-10-218-779-6	Sequence 6, Appli
32	14	3.5	2291	10	US-09-822-871-2	Sequence 2, Appli
33	14	3.5	2291	16	US-10-673-885-2	Sequence 2, Appli
34	14	3.5	2299	16	US-10-466-759-2	Sequence 2, Appli
35	14	3.5	2300	12	US-10-087-684-10	Sequence 10, Appl
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39	14	3.5	2302	12	US-10-087-684-37	Sequence 37, Appl
40	14	3.5	2302	12	US-10-218-779-37	Sequence 37, Appl
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44	12	3.0	1238	15	US-10-366-547-47	Sequence 47, Appl
45	12	3.0	1329	16	US-10-408-765A-2747	Sequence 2747, Ap
46	12	3.0	1337	14	US-10-390-501-2	Sequence 2, Appli
47	12	3.0	1337	15	US-10-366-547-42	Sequence 42, Appl
48	12	3.0	1337	15	US-10-366-547-44	Sequence 44, Appl
49	11	2.7	33	15	US-10-052-648A-85	Sequence 85, Appl
50	11	2.7	98	15	US-10-074-378A-323	Sequence 323, App
51	11	2.7	105	12	US-10-087-684-95	Sequence 95, Appl
52	11	2.7	105	12	US-10-218-779-95	Sequence 95, Appl
53	11	2.7	105	12	US-10-072-012-818	Sequence 818, App
54	11	2.7	248	9	US-09-848-294-10	Sequence 10, Appl
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56	11	2.7	263	12	US-10-087-684-93	Sequence 93, Appl
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62	11	2.7	296	15	US-10-374-499-9	Sequence 9, Appli
63	11	2.7	306	9	US-09-788-626-8	Sequence 8, Appli
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66	11	2.7	309	9	US-09-788-626-12	Sequence 12, Appl
67	11	2.7	310	9	US-09-788-626-10	Sequence 10, Appl
68	11	2.7	310	9	US-09-788-626-15	Sequence 15, Appl
69	11	2.7	312	9	US-09-788-626-24	Sequence 24, Appl
70	11	2.7	312	16	US-10-634-027-6	Sequence 6, Appli
71	11	2.7	313	9	US-09-788-626-7	Sequence 7, Appli
72	11	2.7	313	9	US-03-788-626-17	Sequence 17, Appl
73	11	2.7	316	9	US-09-788-626-5	Sequence 5, Appli
74	11	2.7	316	9	US-09-788-626-26	Sequence 26, Appl
75	11	2.7	317	9	US-09-788-626-4	Sequence 4, Appli
76	11	2.7	319	16	US-10-634-027-7	Sequence 7, Appli
77	11	2.7	336	16	US-10-634-027-4	Sequence 4, Appli
78	11	2.7	341	9	US-09-788-626-23	Sequence 23, Appl
79	11	2.7	454	15	US-10-104-047-2092	Sequence 2092, Ap
80	11	2.7	560	12	US-10-087-192-1020	Sequence 1020, Ap
81	11	2.7	642	16	US-10-444-795B-795	Sequence 795, App
82	11	2.7	659	15	US-10-366-547-67	Sequence 67, Appl
83	11	2.7	699	15	US-10-366-547-65	Sequence 65, Appl
84	11	2.7	700	15	US-10-366-547-63	Sequence 63, Appl
85	11	2.7	700	16	US-10-444-795B-793	Sequence 793, App
86	11	2.7	774	12	US-10-087-192-1017	Sequence 1017, Ap
87	11	2.7	807	15	US-10-264-049-3138	Sequence 3138, Ap
88	11	2.7	962	15	US-10-366-547-85	Sequence 85, Appl

Sequence 4, Appli  
Sequence 1264, Ap  
Sequence 2, Appli  
Sequence 8, Appli  
Sequence 81, Appl  
Sequence 78, Appl  
Sequence 83, Appl  
Sequence 237, App  
Sequence 79, Appl  
Sequence 378, App  
Sequence 1266, Ap  
Sequence 376, App

89 11 2.7 1093 14 US-10-245-539-4  
90 11 2.7 1113 15 US-10-295-027-1264  
91 11 2.7 1118 14 US-10-245-539-2  
92 11 2.7 1118 14 US-10-245-539-8  
93 11 2.7 1143 15 US-10-366-547-81  
94 11 2.7 1188 15 US-10-331-496A-79  
95 11 2.7 1291 15 US-10-366-547-83  
96 11 2.7 1304 15 US-10-116-275-237  
97 11 2.7 1304 15 US-10-366-547-79  
98 11 2.7 1337 15 US-10-295-027-378  
99 11 2.7 1359 15 US-10-295-027-1266  
100 11 2.7 1448 15 US-10-295-027-376

ALIGNMENTS

RESULT 1  
US-09-095-478-3  
; Sequence 3, Application US/09095478  
; Publication No. US20030095970A1

; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, Gregory  
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE SUPTPO5 AND  
; TITLE OF INVENTION: RELATED PRODUCTS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 224/115  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 412 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide

Query Match 100.0%; Score 405; DB 10; Length 412;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMSPRKVRGKGRDNEEGSGNLNLSLPSSSQKMTPTKPIFGNKNSENVPKPSHLL 60  
Db 1 MMSPRKVRGKGRDNEEGSGNLNLSLPSSSQKMTPTKPIFGNKNSENVPKPSHLL 60

QY 61 SFSDKVELYVPEPLESDTDTETVMDVSDRLNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120  
Db 61 SFSDKVELYVPEPLESDTDTETVMDVSDRLNRWNSMDSETAGPSKTVSPVLSGSSRLSK 120  
QY 121 DTTSVSEKELTQLAQIRPLIFNSSARSAMRCLNTLQKKELDIIRBFELEQMTLPDD 180  
Db 121 DTTSVSEKELTQLAQIRPLIFNSSARSAMRCLNTLQKKELDIIRBFELEQMTLPDD 180  
QY 181 FNSGNTLQNRDKNRVRIIDILPYDSTRVPLGNKDYINASYIRIWNHEEYFYATQGPLPE 240  
Db 181 FNSGNTLQNRDKNRVRIIDILPYDSTRVPLGNKDYINASYIRIWNHEEYFYATQGPLPE 240  
QY 241 TIEDFWQVLENNCNVIAMITREIEGVKICSYWPISLKEPLEPEHFSVFLTEHVTQY 300  
Db 241 TIEDFWQVLENNCNVIAMITREIEGVKICSYWPISLKEPLEPEHFSVFLTEHVTQY 300  
QY 301 FTVRVFOIVKSTGKSCQVKHLQFTKMPDHGTGPASADFFIKYVRYVRKSHITGPLLWHCS 360  
Db 301 FTVRVFOIVKSTGKSCQVKHLQFTKMPDHGTGPASADFFIKYVRYVRKSHITGPLLWHCS 360  
QY 361 AGVGTGVPFCVDVWFSATEKNYSFDIMNIVTQMRKQRCMIQTK 405  
Db 361 AGVGTGVPFCVDVWFSATEKNYSFDIMNIVTQMRKQRCMIQTK 405

RESULT 2

US-09-095-478-1  
; Sequence 1, Application US/09095478  
; Publication No. US20030095970A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, Gregory  
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE SUPTPO5 AND  
; TITLE OF INVENTION: RELATED PRODUCTS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 224/115  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide

US-09-095-478-1

Query Match 100.0%; Score 405; DB 10; Length 426;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSPRKVRGTGRDNDDEEGNSGNLNRSLPSSQKMTPTKPIFGNKNNSNVKPSHLL 60  
Db 1 MSSPRKVRGTGRDNDDEEGNSGNLNRSLPSSQKMTPTKPIFGNKNNSNVKPSHLL 60

Qy 61 SFSDKYELVYPEPLESDTDTVDVSDRSRLNRNWSMDSETAGPSKTVSPVLSSGSRSLK 120  
Db 61 SFSDKYELVYPEPLESDTDTVDVSDRSRLNRNWSMDSETAGPSKTVSPVLSSGSRSLK 120

Qy 121 DTETSVSEKLTQAIQIRPLIFNSSARSAMRDCNLTQKKEELDIIREFLEQMTLPDD 180  
Db 121 DTETSVSEKLTQAIQIRPLIFNSSARSAMRDCNLTQKKEELDIIREFLEQMTLPDD 180

Qy 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPE 240  
Db 181 FNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPE 240

Qy 241 TIEDFWMLNENCNVAMITREIECGVTKCYSWPIISLKEPPEFHSVLETFHVQY 300  
Db 241 TIEDFWMLNENCNVAMITREIECGVTKCYSWPIISLKEPPEFHSVLETFHVQY 300

Qy 301 FTVRVFQIVKSTGSKQCVKHLQFTKWPDKGTASADFFIKYVYVRKSHITGPLLHVC 360  
Db 301 FTVRVFQIVKSTGSKQCVKHLQFTKWPDKGTASADFFIKYVYVRKSHITGPLLHVC 360

Qy 361 AGVGRGTVICVDVWFSAIKKNYSFDIMNIVTQMRKORCGMIQ 405  
Db 361 AGVGRGTVICVDVWFSAIKKNYSFDIMNIVTQMRKORCGMIQ 405

## RESULT 3

US-09-095-478-2  
Sequence 2, Application US/09095478  
Publication No. US20030095970A1

GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,478

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 224/115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 463 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-095-478-2

Query Match 89.4%; Score 362; DB 10; Length 463;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 IFGNKNNSNVKPSHLLSFSDKYELVYPEPLESDTDTVDVSDRSRLNRNWSMDSETAG 103  
Db 81 IFGNKNNSNVKPSHLLSFSDKYELVYPEPLESDTDTVDVSDRSRLNRNWSMDSETAG 140

Qy 104 PSKTVSPVLSSGSRSLKDTETSVSEKLTQAIQIRPLIFNSSARSAMRDCNLTQKKEEL 163  
Db 141 PSKTVSPVLSSGSRSLKDTETSVSEKLTQAIQIRPLIFNSSARSAMRDCNLTQKKEEL 200

Qy 164 DIREFLEQMTLPDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIV 223  
Db 201 DIREFLEQMTLPDDFNSGNTLQNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIV 260

Qy 224 NHEEYFYIATQGPLPETIEDFWMLNENCNVAMITREIECGVTKCYSWPIISLKEPL 283  
Db 261 NHEEYFYIATQGPLPETIEDFWMLNENCNVAMITREIECGVTKCYSWPIISLKEPL 320

Qy 284 EFHFSPVLETFHVQYFTVRVFQIVKSTGSKQCVKHLQFTKWPDKGTASADFFIKYV 343  
Db 321 EFHFSPVLETFHVQYFTVRVFQIVKSTGSKQCVKHLQFTKWPDKGTASADFFIKYV 380

Qy 344 RYVRKSHITGPLLHVCAGVGRGTVICVDVWFSAIKKNYSFDIMNIVTQMRKORCGMIQ 403  
Db 381 RYVRKSHITGPLLHVCAGVGRGTVICVDVWFSAIKKNYSFDIMNIVTQMRKORCGMIQ 440

Qy 404 TK 405  
Db 441 TK 442

## RESULT 4

US-09-095-478-8

Sequence 8, Application US/09095478

Publication No. US20030095970A1

GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

TITLE OF INVENTION: NOVEL PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND

TITLE OF INVENTION: RELATED PRODUCTS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,478

FILING DATE:

CLASSIFICATION:





COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-4

Query Match 30.1%; Score 122; DB 10; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.9e-112; Indels 0; Gaps 0;  
Matches 122; Conservative 0; Mismatches 0;  
QY 244 DFWQVLENNCNVIAITREICGVKCYWYPSISLKBELREHPSVLETFHVTQFTV 303  
DB 1 DFWQVLENNCNVIAITREICGVKCYWYPSISLKBELREHPSVLETFHVTQFTV 60  
QY 304 RVFQIVKSTGSKQCVKHLQFTKWDHGPASADFFIKYRVYRKSHITGPLLHCSAGV 363  
DB 61 RVFQIVKSTGSKQCVKHLQFTKWDHGPASADFFIKYRVYRKSHITGPLLHCSAGV 120  
QY 364 GR 365  
DB 121 GR 122

RESULT 7  
US-09-095-478-22  
Sequence 22, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-22

Query Match 7.4%; Score 30; DB 10; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.4e-22; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 0;  
QY 176 TLPDDFNSGNTLQNRDKNRYRDLIPYDSTR 205  
DB 1 TLPDDFNSGNTLQNRDKNRYRDLIPYDSTR 30

RESULT 8  
US-09-095-478-23  
Sequence 23, Application US/09095478  
Publication No. US20030095970A1  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-23

Query Match 7.2%; Score 29; DB 10; Length 29;  
Best Local Similarity 100.0%; Pred. No. 7e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLN 29  
Db 1 MSSPRKVRGKTGRDNDDEEGNSGNLNLN 29

## RESULT 9

US-09-095-478-24  
Sequence 24, Application US/09095478  
Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095.478  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

## FILING DATE:

APPLICANT NUMBER:

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 24:

## SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-24

## Query Match

Best Local Similarity 7.2%; Score 29; DB 10; Length 29;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 SPVLGSSRLSKDTTSVSEKELTOLAQI 137  
Db 1 SPVLGSSRLSKDTTSVSEKELTOLAQI 29

## RESULT 10

US-09-095-478-25  
Sequence 25, Application US/09095478  
Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095.478  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

## FILING DATE:

APPLICANT NUMBER:

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 25:

## SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-25

## Query Match

Best Local Similarity 7.2%; Score 29; DB 10; Length 29;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 WDVSRLRNWNSMDSETAGPSKTVSPV 111

Db 1 WDVSRLRNWNSMDSETAGPSKTVSPV 29

## RESULT 11

US-09-095-478-5  
Sequence 5, Application US/09095478  
Publication No. US20030095970A1

## GENERAL INFORMATION:

APPLICANT: Plowman, Gregory  
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND  
TITLE OF INVENTION: RELATED PRODUCTS AND  
METHODS  
NUMBER OF SEQUENCES: 25

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Past-SEO for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 224/115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-095-478-5

Query Match 5.7%; Score 23; DB 10; Length 122;  
Best Local Similarity 100.0%; Pred. No. 2.2e-14;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 337 DFFIKYRYVRKSHITGFLVHC 359  
Db 94 DFFIKYRYVRKSHITGFLVHC 116

RESULT 12  
US-10-311-764-4  
Sequence 4, Application US/10311764  
Publication No. US20040023245A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
APPLICANT: BAUGHN, Mariah R.; DING, Li  
APPLICANT: ELLIOTT, Vicki S.; GANDHI, Aameena R.  
APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.  
APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
APPLICANT: LU, Yan; NGUYEN, Damiel B.  
APPLICANT: REDDY, Roopa M.; RAMKUNAR, Jayalaxmi  
APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.  
APPLICANT: CHAWLA, Narinder K.; YANG, Junming  
APPLICANT: YAO, Ronique G.; YUE, Henry  
TITLE OF INVENTION: PROTEIN PHOSPHATASES  
FILE REFERENCE: PI-0126 USN  
CURRENT APPLICATION NUMBER: US/10/311,764  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/US01/19442  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/212,447  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US 60/213,746  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/215,210

PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/216,529  
PRIOR FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: US 60/218,080  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/220,117  
PRIOR FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PERL Program  
SEQ ID NO 4  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1  
US-10-311-764-4

Query Match 4.7%; Score 19; DB 16; Length 420;  
Best Local Similarity 100.0%; Pred. No. 6.2e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 KNYRDILPYDSTRVPLGK 210  
Db 186 KNYRDILPYDSTRVPLGK 204

RESULT 13  
US-10-296-115-1082  
Sequence 1082, Application US/10296115  
Publication No. US20040053248A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides  
FILE REFERENCE: 784PCT  
CURRENT APPLICATION NUMBER: US/10/296,115  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 1478  
SEQ ID NO 1082  
LENGTH: 1105  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(1105)  
OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3  
US-10-296-115-1082

Query Match 3.7%; Score 15; DB 12; Length 1105;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 354 PLIVHCSAGVGRGTGV 368  
Db 1015 PLIVHCSAGVGRGTGV 1029

RESULT 14  
US-10-334-143-191  
Sequence 191, Application US/10334143  
Publication No. US20040009549A1  
GENERAL INFORMATION:  
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH  
APPLICANT: SUDARSANAM, SUCHA  
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL  
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD  
FILE REFERENCE: 038602/1543  
CURRENT APPLICATION NUMBER: US/10/334,143  
CURRENT FILING DATE: 2002-12-31

; PRIOR APPLICATION NUMBER: 60/343,169  
 ; PRIOR FILING DATE: 2001-12-31  
 ; NUMBER OF SEQ ID NOS: 207  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 191  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Unknown Organism  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: llara protein sequence  
 US-10-314-232-9

Query Match 3.5%; Score 14; DB 15; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 Db 103 VHCAGVGRGTGVFI 116

RESULT 15  
 US-10-314-232-9  
 ; Sequence 9, Application US/10314232  
 ; Publication No. US20030138932A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOLLER, NIELS P.H.  
 ; APPLICANT: MOLLER, KARIN B.  
 ; APPLICANT: ULLRICH, AXEL  
 ; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
 ; FILE REFERENCE: 038602/0686  
 ; CURRENT APPLICATION NUMBER: US/10/314,232  
 ; CURRENT FILING DATE: 2002-12-09  
 ; PRIOR APPLICATION NUMBER: US/09/361,096  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: 08/449,609  
 ; PRIOR FILING DATE: 1995-05-24  
 ; PRIOR APPLICATION NUMBER: 08/036,210  
 ; PRIOR FILING DATE: 1995-03-23  
 ; NUMBER OF SEQ ID NOS: 53  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 176  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence  
 US-10-314-232-9

Query Match 3.5%; Score 14; DB 14; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 Db 79 VHCAGVGRGTGVFI 92

RESULT 16  
 US-10-314-232-47  
 ; Sequence 47, Application US/10314232  
 ; Publication No. US20030138932A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOLLER, NIELS P.H.  
 ; APPLICANT: MOLLER, KARIN B.  
 ; APPLICANT: ULLRICH, AXEL  
 ; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
 ; FILE REFERENCE: 038602/0686  
 ; CURRENT APPLICATION NUMBER: US/10/314,232  
 ; CURRENT FILING DATE: 2002-12-09  
 ; PRIOR APPLICATION NUMBER: 08/449,609  
 ; PRIOR FILING DATE: 1995-07-26

; PRIOR APPLICATION NUMBER: 08/449,609  
 ; PRIOR FILING DATE: 1995-05-24  
 ; PRIOR APPLICATION NUMBER: 08/036,210  
 ; PRIOR FILING DATE: 1995-03-23  
 ; NUMBER OF SEQ ID NOS: 53  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 47  
 ; LENGTH: 289  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D  
 US-10-314-232-47

Query Match 3.5%; Score 14; DB 14; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 Db 221 VHCAGVGRGTGVFI 234

RESULT 17  
 US-09-788-626-27  
 ; Sequence 27, Application US/09788626  
 ; Patent No. US20020009762A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Flint, Andrew J.  
 ; APPLICANT: COOL, Deborah E.  
 ; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE  
 ; FILE REFERENCE: 200125.401  
 ; CURRENT APPLICATION NUMBER: US/09/788,626  
 ; CURRENT FILING DATE: 2001-02-13  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 27  
 ; LENGTH: 294  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-788-626-27

Query Match 3.5%; Score 14; DB 9; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
 Db 183 VHCAGVGRGTGVFI 196

RESULT 18  
 US-10-314-232-11  
 ; Sequence 11, Application US/10314232  
 ; Publication No. US20030138932A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOLLER, NIELS P.H.  
 ; APPLICANT: MOLLER, KARIN B.  
 ; APPLICANT: ULLRICH, AXEL  
 ; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
 ; FILE REFERENCE: 038602/0686  
 ; CURRENT APPLICATION NUMBER: US/10/314,232  
 ; CURRENT FILING DATE: 2002-12-09  
 ; PRIOR APPLICATION NUMBER: US/09/361,096  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: 08/449,609  
 ; PRIOR FILING DATE: 1995-05-24  
 ; PRIOR APPLICATION NUMBER: 08/036,210  
 ; PRIOR FILING DATE: 1995-03-23  
 ; NUMBER OF SEQ ID NOS: 53  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 11

```
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PTP-S31D
US-10-314-232-11

Query Match          3.5%; Score 14; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370
Db 221 VHCSAGVGRGTGVFI 234

RESULT 19
US-10-408-765A-1670
; Sequence 1670, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Pabv, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1670
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1670

Query Match          3.5%; Score 14; DB 16; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370
Db 274 VHCSAGVGRGTGVFI 287

RESULT 20
US-10-314-232-15
; Sequence 15, Application US/10314232
; Publication No. US20030138932A1
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0686
; CURRENT APPLICATION NUMBER: US/10/314,232
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/361,096
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 401
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-314-232-15

Query Match          3.5%; Score 14; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370
Db 300 VHCSAGVGRGTGVFI 313

RESULT 21
US-09-925-300-950
; Sequence 950, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 950
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-950

Query Match          3.5%; Score 14; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370
Db 372 VHCSAGVGRGTGVFI 385

RESULT 22
US-10-291-265-722
; Sequence 722, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 722
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-722

Query Match          3.5%; Score 14; DB 15; Length 647;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370  
| | | | | | | | | |  
Db 577 VHCSAGVGRGTGVFI 590

RESULT 23  
US-10-314-232-22  
; Sequence 22, Application US/10314232  
; Publication No. US20030138932A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLLER, NIELS P.H.  
; APPLICANT: MOLLER, KARIN B.  
; APPLICANT: ULLRICH, AXEL  
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
; FILE REFERENCE: 038602/0686  
; CURRENT APPLICATION NUMBER: US/10/314,232  
; PRIOR FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US/09/361,096  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: 08/449,609  
; PRIOR FILING DATE: 1995-05-24  
; PRIOR APPLICATION NUMBER: 08/036,210  
; PRIOR FILING DATE: 1995-03-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 898  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PTPS31-RD#2  
US-10-314-232-22

Query Match 3.5%; Score 14; DB 14; Length 898;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370  
| | | | | | | | | |  
Db 797 VHCSAGVGRGTGVFI 810

RESULT 24  
US-10-258-666-12  
; Sequence 12, Application US/10258666  
; Publication No. US20040005578A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, Yoji  
; APPLICANT: Sekine, Susumu  
; APPLICANT: Kikuchi, Yasuhiro  
; APPLICANT: Sakurada, Kazuhiro  
; APPLICANT: Kyowa Hakkō Kogyo Co., Ltd.  
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes  
; FILE REFERENCE: 082382-00000005  
; CURRENT APPLICATION NUMBER: US/10/258,666  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: JP 2000-126741  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: WO PCT/JP01/03700  
; PRIOR FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 1495  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: RHDH-231, PTP-P1  
US-10-258-666-12

Query Match 3.5%; Score 14; DB 15; Length 1495;

Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370  
| | | | | | | | | |  
Db 1426 VHCSAGVGRGTGVFI 1439

RESULT 25  
US-09-808-602-54  
; Sequence 54, Application US/09808602  
; Patent No. US20020155115A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Heriman, John L  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Mezes, Peter S  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: NO. US20020155115alel Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-697 CIP  
; CURRENT APPLICATION NUMBER: US/09/808,602  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 09/800,198  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,596  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 1502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-602-54

Query Match 3.5%; Score 14; DB 9; Length 1502;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTGVFI 370  
| | | | | | | | | |  
Db 1432 VHCSAGVGRGTGVFI 1445

RESULT 26  
US-09-800-198-44  
; Sequence 44, Application US/09800198  
; Publication No. US20030087816A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Cornie AM  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Herrmann, John L  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Rastelli, Luca  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-697  
; CURRENT APPLICATION NUMBER: US/09/800,198  
; CURRENT FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,596  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 1502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-198-44

Query Match 3.5%; Score 14; DB 10; Length 1502;  
Best Local Similarity 100.0%; Pred. No. 0.00018; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
DB 1432 VHCAGVGRGTGVFI 1445

RESULT 27  
US-10-291-265-250  
; Sequence 250, Application US/10291265  
; Publication No. US20030232054A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang et al  
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-017 (785)  
; CURRENT APPLICATION NUMBER: US/10/291,265  
; CURRENT FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 250  
; LENGTH: 1907  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-265-250

Query Match 3.5%; Score 14; DB 15; Length 1907;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
DB 1837 VHCAGVGRGTGVFI 1850

RESULT 28  
US-09-808-602-55  
; Sequence 55, Application US/09808602  
; Patent No. US20020155115A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Heriman, John L  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Mezes, Peter S  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: No. US20020155115A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-697 CIP  
; CURRENT APPLICATION NUMBER: US/09/808,602  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 09/800,198  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,596  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 1948  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-602-55

Query Match 3.5%; Score 14; DB 9; Length 1948;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
DB 1878 VHCAGVGRGTGVFI 1891

RESULT 29  
US-09-800-198-45  
; Sequence 45, Application US/09800198  
; Publication No. US20030087816A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine AM  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Herrmann, John L  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Rastelli, Luca  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-697  
; CURRENT APPLICATION NUMBER: US/09/800,198  
; CURRENT FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,596  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 1948  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-198-45

Query Match 3.5%; Score 14; DB 10; Length 1948;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTGVFI 370  
DB 1878 VHCAGVGRGTGVFI 1891

RESULT 30  
US-10-087-684-6  
; Sequence 6, Application US/10087684  
; Publication No. US20040029116A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Casman, Stacie, J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Guo, Xiaojia





ORGANISM: Human  
US-10-673-885-2

Query Match 3.5%; Score 14; DB 16; Length 2291;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVTGVI 370  
|||||  
DB 2190 VHCAGVGTGVTGVI 2203

## RESULT 34

US-10-466-759-2  
; Sequence 2, Application US/10466759  
; Publication No. US20040081983A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: JACKSON, Jennifer L.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: TRAN, Bao  
; APPLICANT: DING, Li  
; APPLICANT: LU, Dying Aina M.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: WARREN, Bridget A.  
; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
; FILE REFERENCE: PI-0344 USN  
; CURRENT APPLICATION NUMBER: US/10/466,759  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: PCT/US02/01369  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/263,083  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/271,205  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/271,117  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/276,859  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 60/278,504  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/278,522  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/280,510  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 60/280,266  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 2299  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7480588CD1  
US-10-466-759-2

Query Match 3.5%; Score 14; DB 16; Length 2299;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVTGVI 370  
|||||  
DB 2198 VHCAGVGTGVTGVI 2211

## RESULT 35

US-10-087-684-10  
; Sequence 10, Application US/10087684  
; Publication No. US20040029118A1  
; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepiey, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Casman, Stacie, J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gangolli, Bsha A.  
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-214 CIP  
; CURRENT APPLICATION NUMBER: US/10/087,684  
; CURRENT FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 10  
; LENGTH: 2300  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-684-10

Query Match 3.5%; Score 14; DB 12; Length 2300;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGTGVTGVI 370  
|||||  
DB 2199 VHCAGVGTGVTGVI 2212

## RESULT 36

US-10-218-779-10  
; Sequence 10, Application US/10218779  
; Publication No. US20040029222A1  
; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit  
; APPLICANT: MacDougall, John  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen

```

; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Leplev, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-10

Query Match      3.5%; Score 14; DB 12; Length 2300;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCAGVGRGTGVFI 370
Db      2199 VHCAGVGRGTGVFI 2212
|||||

RESULT 37
US-09-822-871-4
; Sequence 4, Application US/09822871
; Publication No. US20030099942A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001219
; CURRENT APPLICATION NUMBER: US/09/822,871
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2301
; TYPE: PRT
; ORGANISM: Rat
US-09-822-871-4

Query Match      3.5%; Score 14; DB 12; Length 2300;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCAGVGRGTGVFI 370
Db      2199 VHCAGVGRGTGVFI 2212
|||||

RESULT 37
US-09-822-871-4
; Sequence 4, Application US/09822871
; Publication No. US20030099942A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001219
; CURRENT APPLICATION NUMBER: US/09/822,871
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2301
; TYPE: PRT
; ORGANISM: Rat
US-09-822-871-4

; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Leplev, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-10

Query Match      3.5%; Score 14; DB 12; Length 2300;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCAGVGRGTGVFI 370
Db      2199 VHCAGVGRGTGVFI 2212
|||||

RESULT 37
US-09-822-871-4
; Sequence 4, Application US/09822871
; Publication No. US20030099942A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001219
; CURRENT APPLICATION NUMBER: US/09/822,871
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2301
; TYPE: PRT
; ORGANISM: Rat
US-09-822-871-4

; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Leplev, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-10

Query Match      3.5%; Score 14; DB 12; Length 2300;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCAGVGRGTGVFI 370
Db      2199 VHCAGVGRGTGVFI 2212
|||||

RESULT 37
US-09-822-871-4
; Sequence 4, Application US/09822871
; Publication No. US20030099942A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001219
; CURRENT APPLICATION NUMBER: US/09/822,871
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2301
; TYPE: PRT
; ORGANISM: Rat
US-09-822-871-4

; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Leplev, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-10

Query Match      3.5%; Score 14; DB 12; Length 2300;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 VHCAGVGRGTGVFI 370
Db      2199 VHCAGVGRGTGVFI 2212
|||||

RESULT 37
US-09-822-871-4
; Sequence 4, Application US/09822871
; Publication No. US20030099942A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION:
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Query Match 3.0%; Score 12; DB 9; Length 319;  
Best Local Similarity 100.0%; Pred. No. 0.0042;  
Matches 12; Conservative 0; Mismatches 0; Indels

QY 356 LVHCSAGVGRGTG 367  
 Db 193 LVHCSAGVGRGTG 204

## RESULT 43

US-10-366-547-49  
 ; Sequence 49, Application US/10366547  
 ; Publication No. US20030215899A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meng, Tzu-Ching  
 ; APPLICANT: Tonks, Nicholas K.  
 ; APPLICANT: Cool, Deborah E.  
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
 ; FILE REFERENCE: 200125.439  
 ; CURRENT APPLICATION NUMBER: US/10/366,547  
 ; CURRENT FILING DATE: 2003-02-12  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 49  
 ; LENGTH: 1216  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-366-547-49

Query Match 3.0%; Score 12; DB 15; Length 1216;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 Db 1115 LVHCSAGVGRGTG 1126

## RESULT 44

US-10-366-547-47  
 ; Sequence 47, Application US/10366547  
 ; Publication No. US20030215899A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meng, Tzu-Ching  
 ; APPLICANT: Tonks, Nicholas K.  
 ; APPLICANT: Cool, Deborah E.  
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
 ; FILE REFERENCE: 200125.439  
 ; CURRENT APPLICATION NUMBER: US/10/366,547  
 ; CURRENT FILING DATE: 2003-02-12  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 47  
 ; LENGTH: 1238  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-366-547-47

Query Match 3.0%; Score 12; DB 15; Length 1238;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 Db 1137 LVHCSAGVGRGTG 1148

## RESULT 45

US-10-408-765A-2747  
 ; Sequence 2747, Application US/10408765A  
 ; Publication No. US20040101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Faly, Eoin D.  
 ; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M. Z.  
 ; APPLICANT: Warnock, Dale Z.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; FILE REFERENCE: 66088.465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2747  
 ; LENGTH: 1329  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123,  
 ; LOCATION: 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135,  
 ; LOCATION: 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147,  
 ; LOCATION: 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 159, 160, 161, 162, 163, 164, 229, 230, 231, 232, 233, 234,  
 ; LOCATION: 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246,  
 ; LOCATION: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258,  
 ; LOCATION: 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281,  
 ; LOCATION: 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293,  
 ; LOCATION: 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305,  
 ; LOCATION: 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 843,  
 ; LOCATION: 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855,  
 ; LOCATION: 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867,  
 ; LOCATION: 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 ; FEATURE:  
 ; NAME/KEY: VARIANT  
 ; LOCATION: 879, 880, 881, 882, 883, 884, 885, 886, 887  
 ; OTHER INFORMATION: Xaa = Any Amino Acid  
 US-10-408-765A-2747

Query Match 3.0%; Score 12; DB 16; Length 1329;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 LVHCSAGVGRGTG 367  
 Db 941 LVHCSAGVGRGTG 952

## RESULT 46

US-10-390-501-2  
 ; Sequence 2, Application US/10390501  
 ; Publication No. US20030148491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tonks, Nicholas K.  
 ; APPLICANT: Ostman, Arne  
 ; TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE  
 ; PHOSPHATASES  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed IP Law Group PLLC  
 ; STREET: Suite 6300, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington

; COUNTRY: USA  
; ZIP: 980104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/390,501  
; FILING DATE: 13-Mar-2003  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rosenman Ph.D., Stephen J.  
; REGISTRATION NUMBER: 43,058  
; REFERENCE/DOCKET NUMBER: 200125.402C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1337 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-390-501-2

Query Match 3.0%; Score 12; DB 14; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 LVHCSAGVGRGTG 367  
Db 1236 LVHCSAGVGRGTG 1247

## RESULT 47

US-10-366-547-42  
; Sequence 42, Application US/10366547  
; Publication No. US20030215899A1  
; GENERAL INFORMATION:  
; APPLICANT: Meng, Tzu-Ching  
; APPLICANT: Tonks, Nicholas K.  
; APPLICANT: Cool, Deborah E.  
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASES  
; FILE REFERENCE: 200125.439  
; CURRENT APPLICATION NUMBER: US/10/366,547  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 1337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-366-547-42

Query Match 3.0%; Score 12; DB 15; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 LVHCSAGVGRGTG 367  
Db 1236 LVHCSAGVGRGTG 1247

## RESULT 48

US-10-366-547-44  
; Sequence 44, Application US/10366547  
; Publication No. US20030215899A1  
; GENERAL INFORMATION:  
; APPLICANT: Meng, Tzu-Ching  
; APPLICANT: Tonks, Nicholas K.

; APPLICANT: Cool, Deborah E.  
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASES  
; FILE REFERENCE: 200125.439  
; CURRENT APPLICATION NUMBER: US/10/366,547  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 1337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-366-547-44

Query Match 3.0%; Score 12; DB 15; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 LVHCSAGVGRGTG 367  
Db 1236 LVHCSAGVGRGTG 1247

## RESULT 49

US-10-052-648A-85  
; Sequence 85, Application US/10052648A  
; Publication No. US20040005558A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Colman, Steven  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Gunther, Erik  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Mehraban, Fuad  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Stone, David J.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF  
; TITLE OF INVENTION: USING THE SAME  
; FILE REFERENCE: 21402-250 (CURA-550)  
; CURRENT APPLICATION NUMBER: US/10/052,648A  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: 60/262,454  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: 60/272,920  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/284,549  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/303,229  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,605  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/269,098  
; PRIOR FILING DATE: 2001-02-15  
; PRIOR APPLICATION NUMBER: 60/264,159  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/271,855  
; PRIOR FILING DATE: 2001-02-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.

PRIOR APPLICATION NUMBER: 60/322,127  
PRIOR FILING DATE: 2001-11-21  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 85  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTPc, Protein  
OTHER INFORMATION: tyrosine phosphatase domain sequence  
US-10-052-649A-85

Query Match 2.7%; Score 11; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred.No. 0.0053;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367  
DB 15 VHCAGVGRTG 25

RESULT 50  
US-10-074-978A-323  
Sequence 323, Application US/10074978A  
Publication No. US20040010119A1  
GENERAL INFORMATION:  
APPLICANT: Leite, Mario  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Fernandes, Elma  
APPLICANT: Li, Li  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Liu, Xiahong  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
APPLICANT: Fatturajan, Meera  
APPLICANT: Bialock, Angela  
APPLICANT: Ballinger, Robert  
APPLICANT: Vernet, Corine  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Malvankar, Uriel M  
APPLICANT: Gusev, Vladimir  
APPLICANT: Rastelli, Luca  
APPLICANT: Mezes, Peter S  
APPLICANT: Ellerman, Karen  
APPLICANT: Heyes, Melvin P  
APPLICANT: Herrman, John  
APPLICANT: Pena, Carol E A  
APPLICANT: Shinkets, Richard A  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Moore, No. US20040010119A1lle  
APPLICANT: Shenoy, Suresh  
APPLICANT: Edinger, Shlomit  
APPLICANT: Gunther, Erik  
APPLICANT: Stone, Dave  
APPLICANT: Millet, Isabelle  
APPLICANT: Peyman, John  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-369  
CURRENT APPLICATION NUMBER: US/10/074, 978A  
CURRENT FILING DATE: 2003-01-07  
PRIORITY APPLICATION NUMBER: 60/268, 221  
PRIOR FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/335, 109  
PRIOR FILING DATE: 2001-10-31  
PRIOR APPLICATION NUMBER: 60/312, 284  
PRIOR FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: 60/268, 496  
PRIOR FILING DATE: 2001-02-13  
PRIOR APPLICATION NUMBER: 60/276, 703  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/330, 293  
PRIOR FILING DATE: 2001-10-18

PRIOR APPLICATION NUMBER: 60/322,127  
PRIOR FILING DATE: 2001-11-21  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 85  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PTPc\_motif  
OTHER INFORMATION: data removed - See File Wrapper or PALM.  
US-10-074-978A-323

Query Match 2.7%; Score 11; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred.No. 0.014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRTG 367  
DB 39 VHCAGVGRTG 49

RESULT 51  
US-10-087-684-95  
Sequence 95, Application US/10087684  
Publication No. US20040029116A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: MacDougall, John R.  
APPLICANT: Millet, Isabelle  
APPLICANT: Ellerman, Karen  
APPLICANT: Stone, David J.  
APPLICANT: Grosse, William M.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Casman, Stacie, J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Li, Li  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Mishra, Vishnu  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Rastelli, Luca  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Malvankar, Uriel M.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Miller, Charles B.  
APPLICANT: Gangolli, Beba A.  
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-214 CIP  
CURRENT APPLICATION NUMBER: US/10/087,684  
CURRENT FILING DATE: 2003-03-10  
PRIORITY APPLICATION NUMBER: 60/253,834  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: 60/250,926  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: 60/264,180  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/274,194  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/313,656  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: 60/327,456  
PRIOR FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 220  
SOFTWARE: Cxaseqdist version 0.1  
SEQ ID NO 95  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Domain  
US-10-087-684-95

Query Match 2.7%; Score 11; DB 12; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
|||||  
Db 44 VHCAGVGRGTG 54

## RESULT 52

US-10-218-779-95

; Sequence 95, Application US/10218779

; Publication No. US20040029222A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit

; APPLICANT: MacDougall, John

; APPLICANT: Millet, Isabelle

; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David

; APPLICANT: Gerlach, Valerie

; APPLICANT: Grosse, William

; APPLICANT: Alsobrook II, John

; APPLICANT: Lepley, Denise

; APPLICANT: Rieger, Daniel

; APPLICANT: Burgess, Catherine

; APPLICANT: Casman, Stacie

; APPLICANT: Spytek, Kimberly

; APPLICANT: Bolog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Mishra, Vishnu

; APPLICANT: Patturajan, Meera

; APPLICANT: Shenoy, Suresh

; APPLICANT: Rastelli, Luca

; APPLICANT: Tchernev, Velizar

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Malyankar, Uriel

; APPLICANT: Guo, Xiaojia

; APPLICANT: Miller, Charles

; APPLICANT: Gangolli, Esha

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-214

; CURRENT APPLICATION NUMBER: US/10/218, 779

; CURRENT FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: 60/253,834

; PRIOR FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 60/250, -926

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: 60/264,180

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 60/313,656

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/327,456

; PRIOR FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 95

; LENGTH: 105

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-218-779-95

Query Match 2.7%; Score 11; DB 12; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCAGVGRGTG 367  
|||||  
Db 44 VHCAGVGRGTG 54

## RESULT 53

US-10-072-012-818

; Sequence 818, Application US/10072012

; Publication No. US20040033493A1

; GENERAL INFORMATION:

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard

; APPLICANT: Li, Li

; APPLICANT: Gangolli, Esha

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Anderson, David W.

; APPLICANT: Rastelli, Luca

; APPLICANT: Miller, Charles E.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Taupier Jr, Raymond J.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Colman, Steven D.

; APPLICANT: Wolenc, Adam R.

; APPLICANT: Pena, Carol E. A

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Grosse, William M.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,517

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,395

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/266,406

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/266,767

; PRIOR FILING DATE: 2001-02-05

; PRIOR APPLICATION NUMBER: 60/267,057

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/267,459

; PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1391

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 818

; LENGTH: 105

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Protein

; OTHER INFORMATION: tyrosine phosphatase, catalytic domain motif

US-10-072-012-818

Query Match 2.7%; Score 11; DB 12; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
|||||  
Db 44 VHCSAGVGRGTG 54

RESULT 54  
US-09-848-294-10  
; Sequence 10, Application US/09848294  
; Patent No. US20020049179A1  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas K.  
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. US20020049179A1e1  
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
; TITLE OF INVENTION: Adhesions and Uses Therefor  
; FILE REFERENCE: CSHL90-042ZA  
; CURRENT APPLICATION NUMBER: US/09/848,294  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 09/235,251  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 08/759,536  
; PRIOR FILING DATE: 1996-12-04  
; PRIOR APPLICATION NUMBER: 08/107,420  
; PRIOR FILING DATE: 1993-08-16  
; PRIOR APPLICATION NUMBER: 07/663,579  
; PRIOR FILING DATE: 1991-03-01  
; PRIOR APPLICATION NUMBER: 07/494,036  
; PRIOR FILING DATE: 1990-03-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-09-848-294-10

Query Match 2.7%; Score 11; DB 9; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
|||||  
Db 175 VHCSAGVGRGTG 185

RESULT 55  
US-10-293-231-10  
; Sequence 10, Application US/10293231  
; Publication No. US20030113294A1  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas K.  
; TITLE OF INVENTION: ISOLATION OF A cDNA ENCODING A NOVEL  
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE WHICH LOCALIZES  
; TITLE OF INVENTION: TO FOCAL ADHESIONS AND USES THEREOF  
; FILE REFERENCE: 200125.409C3  
; CURRENT APPLICATION NUMBER: US/10/293,231  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-231-10

Query Match 2.7%; Score 11; DB 14; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
|||||

Db 175 VHCSAGVGRGTG 185

RESULT 56  
US-10-087-684-93  
; Sequence 93, Application US/10087684  
; Publication No. US20040029116A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Caman, Stacie J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vermet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Malvankar, Uriel M.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gangolli, Esha A.  
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-214 CIP  
; CURRENT APPLICATION NUMBER: US/10/087,684  
; CURRENT FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 93  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Domain  
US-10-087-684-93

Query Match 2.7%; Score 11; DB 12; Length 263;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 VHCSAGVGRGTG 367  
|||||  
Db 201 VHCSAGVGRGTG 211

RESULT 57  
US-10-218-779-93  
; Sequence 93, Application US/10218779  
; Publication No. US20040029222A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit



```

; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shanoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Bsha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-93

Query Match      2.7%; Score 11; DB 12; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
Db      201 VHCSAGVGRGTG 211
|||||

```

```

RESULT 58
US-10-245-539-6
; Sequence 6, Application US/10245539
; Publication No. US20030077639A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR
; FILE REFERENCE: ME101-155P1RM
; CURRENT APPLICATION NUMBER: US/10/245,539
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 60/323,018
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

```

```

; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-245-539-6

Query Match      2.7%; Score 11; DB 14; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
Db      200 VHCSAGVGRGTG 210
|||||

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RESULT 59
US-10-314-232-13
; Sequence 13, Application US/10314232
; Publication No. US20030138932A1
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0686
; CURRENT APPLICATION NUMBER: US/10/314,232
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/361,096
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LAR
US-10-314-232-13

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Query Match      2.7%; Score 11; DB 14; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      231 YIATQGPLPET 241
Db      95 YIATQGPLPET 105
|||||

```

```

RESULT 60
US-10-314-232-12
; Sequence 12, Application US/10314232
; Publication No. US20030138932A1
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0686
; CURRENT APPLICATION NUMBER: US/10/314,232
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/361,096
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1

```

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; SEQ ID NO 12
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CD45
US-10-314-232-12

Query Match          2.7%; Score 11; DB 14; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTG 367
Db 224 VHCAGVGRGTG 234

RESULT 61
US-10-374-539-3
; Sequence 3, Application US/10374539
; Publication No. US20030195247A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: BARR, Kenneth
; APPLICANT: FAHR, Bruce
; APPLICANT: HANSEN, Stig
; APPLICANT: MCDOWELL, Robert
; APPLICANT: WIESMAN, Chris
; APPLICANT: ZHU, Jian
; TITLE OF INVENTION: COMPOUNDS THAT MODULATE THE ACTIVITY OF
; FILE REFERENCE: 39750-0008
; CURRENT APPLICATION NUMBER: US/10/374,539
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/361,475
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-539-3

Query Match          2.7%; Score 11; DB 14; Length 296;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 YIATQGPLPET 241
Db 88 YIATQGPLPET 98

RESULT 62
US-10-374-499-9
; Sequence 9, Application US/10374499
; Publication No. US20040005632A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: ERLANSON, Daniel A.
; APPLICANT: MCDOWELL, Robert S.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
; FILE REFERENCE: 39750-0016
; CURRENT APPLICATION NUMBER: US/10/374,499
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/377,034
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 10/121,216
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9

Query Match          2.7%; Score 11; DB 14; Length 296;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 YIATQGPLPET 241
Db 88 YIATQGPLPET 98

RESULT 63
US-09-788-626-8
; Sequence 8, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-8

Query Match          2.7%; Score 11; DB 9; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 YIATQGPLPET 241
Db 57 YIATQGPLPET 67

RESULT 64
US-09-788-626-25
; Sequence 25, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Schizosaccaromyces pombe
US-09-788-626-25

Query Match          2.7%; Score 11; DB 9; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 VHCAGVGRGTG 367
Db 180 VHCAGVGRGTG 190

RESULT 65
```

```
US-09-788-626-11
; Sequence 11, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-11

Query Match      2.7%; Score 11; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
      |||||
Db      184 VHCSAGVGRGTG 194

RESULT 66
US-09-788-626-12
; Sequence 12, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-626-12

Query Match      2.7%; Score 11; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
      |||||
Db      184 VHCSAGVGRGTG 194

RESULT 67
US-09-788-626-10
; Sequence 10, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-10

Query Match      2.7%; Score 11; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
      |||||
Db      185 VHCSAGVGRGTG 195

RESULT 68
US-09-788-626-15
; Sequence 15, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-15

Query Match      2.7%; Score 11; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
      |||||
Db      185 VHCSAGVGRGTG 195

RESULT 69
US-09-788-626-24
; Sequence 24, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Schizosaccaromyces pombe
US-09-788-626-24

Query Match      2.7%; Score 11; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 VHCSAGVGRGTG 367
      |||||
Db      183 VHCSAGVGRGTG 193

RESULT 70
US-10-634-027-6
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